

STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 106579

TO: James Schultz
Location: cm1/12e18/11e12
Art Unit: 1635
Wednesday, October 29, 2003

Case Serial Number: 09331204

From: Toby Port
Location: Biotech-Chem Library
CM1-6A04
Phone: 308-3534

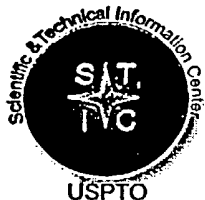
toby.port@uspto.gov

Search Notes

Dear Examiner Schultz,

Here are the results of your search.
Please feel free to contact me if you have any questions.

Toby Port



STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher* or *contact*:

Mary Hale, Information Branch Supervisor
308-4258, CM1-1E01

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library CM1 - Circ. Desk



106579

STIC-Biotech/ChemLib

From: Schultz, James
Sent: Thursday, October 23, 2003 9:39 AM
To: STIC-Biotech/ChemLib
Subject: Seq Search request 09/331,204

Hello,

Could you please perform a length limited nucleotide sequence search against SEQ ID NOS: 4-8 and 13 in the above entitled application, where the maximum size of the returned hit is no longer than 22 nucleotides? SEQ ID NOS: 4, 5, 7, and 8 are 18mers, SEQ ID NO: 6 is a 21mer, and SEQ ID NO: 13 is a 12mer. This application recited multiple sequences as originally filed, before we started restricting to one sequence. Also, I need the interference databases searched.

Thanks,
Doug Schultz

J. Douglas Schultz, Ph.D.
AU 1635 (Biotechnology)
Patent Examiner
United States Patent and Trademark Office
(703) 308-9355
(703) 746-3973 (fax)
Office: CM1 12E18
Mail: CM1 11E12

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 11:09:34 ; Search time 307.029 Seconds
(without alignments)
97.777 Million cell updates/sec

Title: US-09-331-204A-4

Perfect score: 18

Sequence: 1 ttggaggggggtggggg 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2231628 seqs, 833900706 residues

Total number of hits satisfying chosen parameters: 264402

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents NA New.*

- 1: /cgn2_6/ptodata1/pna/PCT_NEW_COMB.seq.*
- 2: /cgn2_6/ptodata1/pna/US05_NEW_COMB.seq.*
- 3: /cgn2_6/ptodata1/pna/US07_NEW_COMB.seq.*
- 4: /cgn2_6/ptodata1/pna/US08_NEW_COMB.seq.*
- 5: /cgn2_6/ptodata1/pna/US09_NEW_COMB.seq.*
- 6: /cgn2_6/ptodata1/pna/US10_NEW_COMB.seq.*
- 7: /cgn2_6/ptodata1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14.4	80.0	18	1	PCT-US02-38216-41647 Sequence 41647, A
2	14.4	80.0	19	1	PCT-US02-38216-38943 Sequence 38943, A
3	14.4	80.0	19	1	PCT-US02-38216-46976 Sequence 46976, A
4	14.4	80.0	22	1	PCT-US02-38216-26689 Sequence 26689, A
5	14.4	80.0	22	1	PCT-US02-38216-42141 Sequence 42141, A
6	14.4	77.8	18	1	PCT-US02-38216-27376 Sequence 27376, A
7	14.4	77.8	19	1	PCT-US02-38216-27360 Sequence 27360, A
8	13.8	76.7	19	1	PCT-US02-38216-18278 Sequence 18278, A
9	13.8	76.7	19	1	PCT-US02-38216-47426 Sequence 47426, A
10	13.8	76.7	19	1	PCT-US02-38216-61865 Sequence 61865, A
11	13.8	76.7	20	1	PCT-US02-38216-18418 Sequence 18418, A
12	13.8	76.7	20	1	PCT-US02-38216-39237 Sequence 39237, A
13	13.8	76.7	21	1	PCT-US02-38216-11847 Sequence 11847, A
14	13.8	76.7	21	1	PCT-US02-38216-75562 Sequence 75562, A
15	13.8	76.7	22	1	PCT-US02-38216-63940 Sequence 63940, A
16	13.4	74.4	18	1	PCT-US02-38216-38927 Sequence 38927, A
17	13.4	74.4	19	1	PCT-US02-38216-53577 Sequence 53577, A
18	13.4	74.4	19	1	PCT-US02-38216-78687 Sequence 78687, A
19	13.4	74.4	20	1	PCT-US02-38216-41804 Sequence 41804, A
20	13.4	74.4	20	5	US-09-978-3338-2 Sequence 2, Appli
21	13.4	74.4	20	5	US-09-978-3338-2 Sequence 2, Appli
22	13.4	74.4	21	1	PCT-US02-38216-41967 Sequence 41967, A
23	13.4	74.4	21	1	PCT-US02-38216-55622 Sequence 55622, A
24	13.4	74.4	21	1	PCT-US02-38216-57364 Sequence 57364, A
25	13.4	74.4	21	1	PCT-US02-38216-78761 Sequence 78761, A
26	13.4	74.4	22	1	PCT-US02-38216-39492 Sequence 39492, A

ALIGNMENTS

RESULT 1

PCT-US02-38216-41647
; Sequence 41647, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 41647
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-41647

Query Match 80.0%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGAGGGGGTGGTGGG 18
Db 1 GGAGGGGGTGGAGGGG 16

RESULT 2

PCT-US02-38216-38943
; Sequence 38943, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 38943
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-38943

Query Match 80.0%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Sequence 51896, A
Sequence 86378, A
Sequence 68852, A
Sequence 57248, A
Sequence 4725, Ap
Sequence 4726, Ap
Sequence 5015, Ap
Sequence 5016, Ap
Sequence 9770, Ap
Sequence 70363, A
Sequence 76556, A
Sequence 86654, A
Sequence 9675, Ap
Sequence 9731, Ap
Sequence 29535, A
Sequence 36098, A
Sequence 41599, A
Sequence 51842, A
Sequence 60928, A

QY 3 GGAGGGGGTGGTGGG 18
|||||
Db 4 GGAGGGGGTGGTGGG 19

RESULT 3
PCT-US02-38216-46976
; Sequence 46976, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46976
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-46976

Query Match 80.0%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGGGGTGGTGGG 18
|||||
Db 4 GGTGGGGTGGTGGG 19

RESULT 4
PCT-US02-38216-26689/c
; Sequence 26689, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26689
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-26689

Query Match 80.0%; Score 14.4; DB 1; Length 22;
Best Local Similarity 93.8%; Pred. No. 9.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGTGGTGG 16
|||||
Db 16 TTGGAGGAGGTGGTGG 1

RESULT 5
PCT-US02-38216-42141
; Sequence 42141, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42141
; LENGTH: 22

; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-42141

Query Match 80.0%; Score 14.4; DB 1; Length 22;
Best Local Similarity 93.8%; Pred. No. 9.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGGGGTGGTGGG 18
|||||
Db 2 GGTGGGGTGGTGGG 17

RESULT 6
PCT-US02-38216-27376
; Sequence 27376, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27376
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-27376

Query Match 77.8%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGAGGGGGTGGTG 15
|||||
Db 3 TGGAGGGGGTGGTG 16

RESULT 7
PCT-US02-38216-27360
; Sequence 27360, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27360
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-27360

Query Match 77.8%; Score 14; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGAGGGGGTGGTGG 16
|||||
Db 5 GGAGGGGGTGGTGG 18

RESULT 8
PCT-US02-38216-18278
; Sequence 18278, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY

; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18278
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-18278

Query Match 76.7%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.7e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTGAGGGGGTGTGGG 17
Db 1 TGGAGGGGGTGGAGG 17

RESULT 9
PCT-US02-38216-47426
; Sequence 47426, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47426
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-47426

Query Match 76.7%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.7e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGGAGGGGGTGTGGG 18
Db 3 TGGAGGGGGAGGAGG 19

RESULT 10
PCT-US02-38216-61865/c
; Sequence 61865, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61865
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-61865

Query Match 76.7%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.7e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGGAGGGGGTGTGGG 18
Db 17 TGGACGGGGTGTGGT 1

RESULT 11
PCT-US02-38216-18418
; Sequence 18418, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18418
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-18418

Query Match 76.7%; Score 13.8; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.7e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGGAGGGGGTGTGGG 18
Db 1 TGGAGGGGGTGGGAGG 17

RESULT 12
PCT-US02-38216-39237
; Sequence 39237, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39237
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-39237

Query Match 76.7%; Score 13.8; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.7e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGGAGGGGGTGTGGG 18
Db 4 TGGAGGTAGTGTGGGG 20

RESULT 13
PCT-US02-38216-51847
; Sequence 51847, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51847
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-51847

Query Match 76.7%; Score 13.8; DB 1; Length 21;
Best Local Similarity 88.2%; Pred. No. 1.6e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGAGGGGGTGGTGGG 18
DB 4 TGGTGGGGCGGTGGG 20

RESULT 14
PCT-US02-38216-75562
; Sequence 75562, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 75562
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-75562

Query Match 76.7%; Score 13.8; DB 1; Length 21;
Best Local Similarity 88.2%; Pred. No. 1.6e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGAGGGGGTGGTGGG 18
DB 1 TGCAGGGGGTGGTGGAG 17

RESULT 15
PCT-US02-38216-63940
; Sequence 63940, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63940
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-63940

Query Match 76.7%; Score 13.8; DB 1; Length 22;
Best Local Similarity 88.2%; Pred. No. 1.6e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGAGGGGGTGGTGGG 18
DB 3 TGGGGGGGGTGGGGGGG 19

Search completed: October 27, 2003, 18:22:55
Job time : 308.029 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:35 ; Search time 2356.29 Seconds
(without alignments)
253.343 Million cell updates/sec

Title: US-09-331-204A-4
Perfect score: 18
Sequence: 1 ttggagggggtggtggg 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Capext 1.0

Searched: 33363688 seqs, 1658188974 residues

Total number of hits satisfying chosen parameters: 2938060

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_NA_Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	8	US-08-387-041A-3
2	18	100.0	18	19	US-09-331-204-1
3	18	100.0	18	19	US-09-331-204A-4
4	18	100.0	18	33	US-09-786-436-17

5 18 100.0 18 33 US-09-786-436-42 Sequence 42, Appl
6 18 100.0 21 8 US-08-387-041A-4 Sequence 4, Appl
7 18 100.0 21 19 US-09-331-204A-6 Sequence 6, Appl
8 18 100.0 21 19 US-09-331-204A-6 Sequence 6, Appl
9 16.4 91.1 18 19 US-09-331-204A-8 Sequence 5, Appl
10 16.4 91.1 18 19 US-09-331-204A-8 Sequence 5, Appl
11 14.8 82.2 18 19 US-09-331-204A-7 Sequence 7, Appl
12 14.8 82.2 18 19 US-09-331-204A-9 Sequence 9, Appl
13 14.8 82.2 18 19 US-09-331-204A-4 Sequence 4, Appl
14 14.4 80.0 18 50 US-10-310-188-41647 Sequence 41647, A
15 14.4 80.0 19 50 US-10-310-188-38943 Sequence 38943, A
16 14.4 80.0 19 50 US-10-310-188-46976 Sequence 46976, A
17 14.4 80.0 22 50 US-10-310-188-26689 Sequence 26689, A
18 14.4 80.0 22 50 US-10-310-188-42141 Sequence 42141, A
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24 13.8 76.7 20 50 US-10-310-188-18418 Sequence 18418, A
25 13.8 76.7 20 50 US-10-310-188-39237 Sequence 39237, A
26 13.8 76.7 21 50 US-10-310-188-51847 Sequence 51847, A
27 13.8 76.7 21 50 US-10-310-188-75562 Sequence 75562, A
28 13.8 76.7 22 9 US-08-472-801-186 Sequence 186, App
29 13.8 76.7 22 9 US-08-472-801-2653 Sequence 2653, App
30 13.8 76.7 22 9 US-08-472-801-2660 Sequence 2660, App
31 13.8 76.7 22 11 US-08-668-235-186 Sequence 186, App
32 13.8 76.7 22 11 US-08-668-235-2653 Sequence 2653, App
33 13.8 76.7 22 11 US-08-668-235-2660 Sequence 2660, App
34 13.8 76.7 22 47 US-10-160-499-186 Sequence 186, App
35 13.8 76.7 22 47 US-10-160-499-2653 Sequence 2653, App
36 13.8 76.7 22 47 US-10-160-499-2660 Sequence 2660, App
37 13.8 76.7 22 50 US-10-310-188-63940 Sequence 63940, A
38 13.6 75.6 22 42 US-09-979-666B-79 Sequence 79, Appl
39 13.4 74.4 15 1 PCT-US01-12255-8 Sequence 8, Appl
40 13.4 74.4 15 2 PCT-US01-12255-8 Sequence 8, Appl
41 13.4 74.4 16 50 US-10-303-778-1282 Sequence 1282, App
42 13.4 74.4 18 50 US-10-310-188-38927 Sequence 38927, A
43 13.4 74.4 19 49 US-10-293-328-6664 Sequence 6664, App
44 13.4 74.4 19 50 US-10-310-188-53577 Sequence 53577, A
45 13.4 74.4 19 50 US-10-310-188-78687 Sequence 78687, A

ALIGNMENTS

RESULT 1
US-08-387-041A-3
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATION
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,041A
; FILING DATE: 02-FEB-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227

; REFERENCE/DOCKET NUMBER: 8250-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; US-08-387-041A-3

Query Match 100.0%; Score 18; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGTGGTGGG 18
Db 1 TTGGAGGGGGTGGTGGG 18

RESULT 2

US-09-331-204-1
; Sequence 1, Application US/09331204
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert

; TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN
; TITLE OF INVENTION: IMMUNE RESPONSE
; FILE REFERENCE: ICNSequence
; CURRENT APPLICATION NUMBER: US/09/331,204
; PRIOR FILING DATE: 1999-08-20
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: An oligomer
; OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic
; OTHER INFORMATION: acid including oligomers consisting of naturally
; OTHER INFORMATION: occurring bases, sugars and intersugar
; US-09-331-204-1

Query Match 100.0%; Score 18; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGTGGTGGG 18
Db 1 TTGGAGGGGGTGGTGGG 18

RESULT 3

US-09-331-204A-4
; Sequence 4, Application US/09331204A
; GENERAL INFORMATION:
; APPLICANT: ICN Pharmaceuticals, Inc.

; TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Res
; FILE REFERENCE: 216/013-US1
; CURRENT APPLICATION NUMBER: US/09/331,204A
; CURRENT FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US97/23927
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 18

TYPE: DNA
ORGANISM: synthetic construct
US-09-331-204A-4

Query Match 100.0%; Score 18; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGTGGTGGG 18
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Db 1 TTGGAGGGGGTGGTGGG 18

RESULT 4
US-09-786-436-17
Sequence 17, Application US/09786436
GENERAL INFORMATION:
APPLICANT: Wagner, Hermann
APPLICANT: Lipford, Grayson
APPLICANT: Heeg, Klaus
TITLE OF INVENTION: G-Motif Oligonucleotides and Uses
FILE REFERENCE: C1041/7010 (AWS)
CURRENT APPLICATION NUMBER: US/09/786,436
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: PCT/EP99/06502
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 17
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
US-09-786-436-17

Query Match 100.0%; Score 18; DB 33; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGTGGTGGG 18
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Db 1 TTGGAGGGGGTGGTGGG 18

RESULT 5
US-09-786-436-42/c
Sequence 42, Application US/09786436
GENERAL INFORMATION:
APPLICANT: Wagner, Hermann
APPLICANT: Lipford, Grayson
APPLICANT: Heeg, Klaus
TITLE OF INVENTION: G-Motif Oligonucleotides and Uses
FILE REFERENCE: C1041/7010 (AWS)
CURRENT APPLICATION NUMBER: US/09/786,436
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: PCT/EP99/06502
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 42
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
US-09-786-436-42

Query Match 100.0%; Score 18; DB 33; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 18 TTGGAGGGGGTGGTGGG 1
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RESULT 6
US-08-387-041A-4
Sequence 4, Application US/08387041A
GENERAL INFORMATION:
APPLICANT: Tam, Robert C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATION
OF CD28 EXPRESSION
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,041A
FILING DATE: 02-FEB-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8250-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-387-041A-4

Query Match 100.0%; Score 18; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGTGGTGGG 18
|||||
Db 4 TTGGAGGGGGTGGTGGG 21

RESULT 7
US-09-331-204-6
Sequence 6, Application US/09331204
GENERAL INFORMATION:
APPLICANT: Tam, Robert
TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN
IMMUNE RESPONSE
FILE REFERENCE: ICNSequence
CURRENT APPLICATION NUMBER: US/09/331,204
CURRENT FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: PCT/US97/23927
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 21
TYPE: DNA

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: An oligomer
; OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic
; OTHER INFORMATION: acid. This term includes oligomers consisting of
; OTHER INFORMATION: naturally occurring bases, sugars and intersugar (
US-09-331-204-6
Query Match      100.0%; Score 18; DB 19; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGTGGTGGGG 18
Db 4 TTGGAGGGGGTGGTGGGG 21

RESULT 8
US-09-331-204A-6
; Sequence 6, Application US/09331204A
; GENERAL INFORMATION:
; APPLICANT: ICN Pharmaceuticals, Inc.
; APPLICANT: Tam, Robert
; TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Respo
; FILE REFERENCE: 216/013-US1
; CURRENT APPLICATION NUMBER: US/09/331,204A
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US97/23927
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 21
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-331-204A-6

Query Match      100.0%; Score 18; DB 19; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGTGGTGGGG 18
Db 4 TTGGAGGGGGTGGTGGGG 21

RESULT 9
US-09-331-204-5
; Sequence 5, Application US/09331204
; GENERAL INFORMATION:
; APPLICANT: ICN Pharmaceuticals, Inc.
; APPLICANT: Tam, Robert
; TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN
; FILE REFERENCE: ICNSequence
; CURRENT APPLICATION NUMBER: US/09/331,204
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US97/23927
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: An oligomer
; OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic
; OTHER INFORMATION: acid. This term includes oligomers consisting of
; OTHER INFORMATION: naturally occurring bases, sugars and intersugar (
US-09-331-204-5

Query Match      91.1%; Score 16.4; DB 19; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.9e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGTGGTGGGG 18
Db 1 TTGGAGGGGGAGGTGGGG 18

RESULT 10
US-09-331-204A-8
; Sequence 8, Application US/09331204A
; GENERAL INFORMATION:
; APPLICANT: ICN Pharmaceuticals, Inc.
; APPLICANT: Tam, Robert
; TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Res;
; FILE REFERENCE: 216/013-US1
; CURRENT APPLICATION NUMBER: US/09/331,204A
; CURRENT FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US97/23927
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 18
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-331-204A-8

Query Match      91.1%; Score 16.4; DB 19; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.9e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGTGGTGGGG 18
Db 1 TTGGAGGGGGAGGTGGGG 18

RESULT 11
US-09-331-204A-7
; Sequence 7, Application US/09331204A
; GENERAL INFORMATION:
; APPLICANT: ICN Pharmaceuticals, Inc.
; APPLICANT: Tam, Robert
; TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Res;
; FILE REFERENCE: 216/013-US1
; CURRENT APPLICATION NUMBER: US/09/331,204A
; CURRENT FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US97/23927
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 18
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-331-204A-7

Query Match      82.2%; Score 14.8; DB 19; Length 18;
Best Local Similarity 88.9%; Pred. No. 7.8e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGTGGTGGGG 18
Db 1 TTGGAGGGGGAGGTGGGG 18

RESULT 12
US-09-331-204A-9
; Sequence 9, Application US/09331204A
; GENERAL INFORMATION:
; APPLICANT: ICN Pharmaceuticals, Inc.
; APPLICANT: Tam, Robert
; TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Res;
; FILE REFERENCE: 216/013-US1
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; CURRENT APPLICATION NUMBER: US/09/331.204A
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US97/23927
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 18
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-331-204A-9

Query Match 82.2%; Score 14.8; DB 19; Length 18;
Best Local Similarity 88.9%; Pred. No. 7.8e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTGAGGGGGTGGTGGGG 18
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Db 1 TTGAGGGGGTGGTGGGG 18

RESULT 13
US-09-331-204-4
; Sequence 4, Application US/09331.204
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert
; TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN
; FILE REFERENCE: ICNSequence
; CURRENT APPLICATION NUMBER: US/09/331.204
; CURRENT FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US97/23927
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: An oligomer
; OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic
; OTHER INFORMATION: acid. This term includes oligomers consisting of
; OTHER INFORMATION: naturally occurring bases, sugars and intersugar (

Query Match 82.2%; Score 14.8; DB 19; Length 19;
Best Local Similarity 88.9%; Pred. No. 7.8e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTGAGGGGGTGGTGGGG 18
| | | | | | | | | | | | | | | | | |
Db 1 TTGAGGGGGGAGGAGGGG 18

RESULT 14
US-10-310-188-41647
; Sequence 41647, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310.188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41647
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-41647

Query Match 80.0%; Score 14.4; DB 50; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGAGGGGGTGGTGGGG 18
| | | | | | | | | | | | | | | | | |
Db 1 GGAGGGGGTGGAGGGG 16

RESULT 15
US-10-310-188-38943
; Sequence 38943, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310.188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38943
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-38943

Query Match 80.0%; Score 14.4; DB 50; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGAGGGGGTGGTGGGG 18
| | | | | | | | | | | | | | | | | |
Db 4 GGAGGGGGTGGCGGGG 19

Search completed: October 27, 2003, 17:52:51
Job time : 2357.29 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 11:25:34 ; Search time 387.943 Seconds
(without alignments)
124.432 Million cell updates/sec

Title: US-09-331-204A-4
Perfect score: 18
Sequence: 1 ttggagggtgtgtggg 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1792395 seqs, 134090451 residues

Total number of hits satisfying chosen parameters: 408622

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*

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12: /cgn2_6/ptodata1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata1/pubpna/US10_NEW_PUB.seq.*
16: /cgn2_6/ptodata1/pubpna/US60_NEW_PUB.seq.*
17: /cgn2_6/ptodata1/pubpna/US60_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	13.4	74.4	20	10	US-09-874-162A-22
C 2	13	72.2	17	11	US-09-740-332-2132
C 3	13	72.2	17	11	US-09-740-332-2133
C 4	13	72.2	17	11	US-09-740-332-2422
C 5	13	72.2	17	11	US-09-740-332-2423
C 6	13	72.2	17	12	US-09-817-879-2132
C 7	13	72.2	17	12	US-09-817-879-2133
C 8	13	72.2	17	12	US-09-817-879-2422
C 9	13	72.2	17	12	US-09-817-879-2423
C 10	12.8	71.1	17	12	US-10-059-877-26
C 11	12.8	71.1	17	12	US-10-303-109A-30
C 12	12.8	71.1	17	14	US-10-059-888-26
C 13	12.8	71.1	20	14	US-10-181-846-35
C 14	12.8	71.1	22	11	US-09-988-115A-3
C 15	12.8	71.1	22	11	US-09-988-115A-13
C 16	12.8	71.1	22	11	US-09-988-115A-20

C 17	12.8	71.1	22	11	US-09-988-115A-22
C 18	12.4	68.9	20	12	US-10-032-985-5333
C 19	12.2	67.8	17	10	US-09-263-959-904
C 20	12.2	67.8	18	14	US-10-196-460-4
C 21	12.2	67.8	19	12	US-10-318-628-9
C 22	12.2	67.8	20	9	US-09-854-983-174
C 23	12.2	67.8	20	10	US-09-755-004-10
C 24	12.2	67.8	20	11	US-09-779-152-56
C 25	12.2	67.8	20	12	US-09-767-421-36
C 26	12.2	67.8	20	14	US-10-023-610-56
C 27	12.2	67.8	21	9	US-09-828-034-11
C 28	12.2	67.8	21	9	US-09-828-034-30
C 29	12.2	67.8	21	9	US-09-828-034-31
C 30	12	66.7	18	12	US-10-204-884-59
C 31	11.8	65.6	16	12	US-10-059-877-22
C 32	11.8	65.6	16	14	US-10-059-888-22
C 33	11.8	65.6	17	10	US-09-263-959-900
C 34	11.8	65.6	17	11	US-09-930-423-522
C 35	11.8	65.6	17	11	US-09-930-423-523
C 36	11.8	65.6	17	12	US-09-745-237A-522
C 37	11.8	65.6	17	12	US-09-745-237A-523
C 38	11.8	65.6	17	12	US-10-061-201-1934
C 39	11.8	65.6	17	12	US-10-061-201-1935
C 40	11.8	65.6	17	12	US-10-061-201-1936
C 41	11.8	65.6	18	10	US-09-263-959-921
C 42	11.8	65.6	18	11	US-09-846-033B-117
C 43	11.8	65.6	18	14	US-10-006-069A-117
C 44	11.8	65.6	19	14	US-10-010-920-67
C 45	11.8	65.6	19	14	US-10-008-721-67

ALIGNMENTS

RESULT 1
US-09-874-162A-22/c
; Sequence 22, Application US/09874162A
; Patent No. US20020155452A1
; GENERAL INFORMATION:
; APPLICANT: Koontz, Jason
; APPLICANT: Sklar, Jeffrey
; TITLE OF INVENTION: FUSION OF JAZF1 AND JAZZ1 GENES IN
; TITLE OF INVENTION: ENDOMETRIAL STROMAL TUMORS
; FILE REFERENCE: 05311-024001
; CURRENT APPLICATION NUMBER: US/09/874.162A
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 60/209,093
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for PCR
US-09-874-162A-22

Query Match 74.4%; Score 13.4; DB 10; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGGGGTGGTGGG 17
| | | | | | | | | | | | | | | | | | | | | |
DB 19 GGAGGGGGTGGTGGG 5

RESULT 2
US-09-740-332-2132/c
; Sequence 2132, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.

```
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2132
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-2132

Query Match          72.2%; Score 13; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GGGGGTGGTGGG 18
        |||||
Db      17 GGGGGTGGTGGG 5

RESULT 3
US-09-740-332-2133/c
; Sequence 2133, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2133
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-2133

Query Match          72.2%; Score 13; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GGGGGTGGTGGG 18
        |||||
Db      14 GGGGGTGGTGGG 2

RESULT 4
US-09-740-332-2422
; Sequence 2422, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2422
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-2132/c
; Sequence 2132, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; FILE REFERENCE: MBHB00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2132
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-2132

Query Match          72.2%; Score 13; DB 12; Length 17;
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; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-2422

Query Match          72.2%; Score 13; DB 11; Length 17;
Best Local Similarity 84.6%; Pred. No. 2e+04;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      6 GGGGGTGGTGGG 18
        |||||
Db      5 GGGGGUGUGUGGG 17

RESULT 5
US-09-740-332-2423
; Sequence 2423, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2423
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-2423

Query Match          72.2%; Score 13; DB 11; Length 17;
Best Local Similarity 84.6%; Pred. No. 2e+04;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      6 GGGGGTGGTGGG 18
        |||||
Db      2 GGGGGUGUGUGGG 14

RESULT 6
US-09-817-879-2132/c
; Sequence 2132, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; FILE REFERENCE: MBHB00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2132
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-2132

Query Match          72.2%; Score 13; DB 12; Length 17;
```

```
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGGGCTGCTGGG 18
    |||||
Db 17 GGGGCTGCTGGG 5

RESULT 7
US-09-817-879-2133/c
; Sequence 2133, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MHB00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2133
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-2133

Query Match 72.2%; Score 13; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGGGCTGCTGGG 18
    |||||
Db 14 GGGGCTGCTGGG 2

RESULT 8
US-09-817-879-2422
; Sequence 2422, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MHB00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2422
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-2422

Query Match 72.2%; Score 13; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGGGCTGCTGGG 18
    |||||
Db 5 GGGGCTGCTGGG 17

RESULT 9
US-09-817-879-2423
; Sequence 2423, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MHB00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2423
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-2423

Query Match 72.2%; Score 13; DB 12; Length 17;
Best Local Similarity 84.6%; Pred. No. 2e+04;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGGGCTGCTGGG 18
    |||||
Db 2 GGGGCTGCTGGG 14

RESULT 10
US-10-059-877-26
; Sequence 26, Application US/10059877
; Publication No. US20030157490A1
; GENERAL INFORMATION:
; APPLICANT: CHAO, JULIE
; APPLICANT: SONG, QING
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING
; TITLE OF INVENTION: TISSUE KALLIKREIN GENE PROMOTER POLYMORPHISMS WITH ESSENTIAL
; FILE REFERENCE: 19113.0081U2
; CURRENT APPLICATION NUMBER: US/10/059,877
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: 09/495,140
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 09/389,566
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 08/856,141
; PRIOR FILING DATE: 1997-05-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: /No. US20030157490A1 =
; OTHER INFORMATION: Synthetic construct
US-10-059-877-26

Query Match 71.1%; Score 12.8; DB 12; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGAGGGGCTGCTGGG 18
    |||||
Db 1 GGAGGGGCTGCTGGG 16

RESULT 11
US-10-303-109A-30/c
```

; Sequence 30, Application US/10303109A
; Publication No. US20030194726A1
; GENERAL INFORMATION:
; APPLICANT: BOLCHAKOVA, Elena
; TITLE OF INVENTION: Thermus Oshimai Nucleic Acid Polymerases
; FILE REFERENCE: 4777US
; CURRENT APPLICATION NUMBER: US/10/303,109A
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/334,798
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Thermus oshimai
US-10-303-109A-30

Query Match 71.1%; Score 12.8; DB 12; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGAGGGGTGGTGGG 17
||||| |||||
DB 16 TGGAGGTGGAGTGGG 1

RESULT 12

US-10-059-888-26
; Sequence 26, Application US/10059888
; Publication No. US20030025882A1
; GENERAL INFORMATION:
; APPLICANT: CHAO, LEE
; APPLICANT: CHAO, JULIE
; APPLICANT: SONG, QING
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING
; TITLE OF INVENTION: TISSUE KALLIKREIN GENE PROMOTER POLYMORPHISMS WITH ESSENTIAL
; FILE REFERENCE: 19113.0081U2
; CURRENT APPLICATION NUMBER: US/10/059,888
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: 09/495,140
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 09/389,566
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 08/856,141
; PRIOR FILING DATE: 1997-05-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence./No. US20030025882A1e =
; OTHER INFORMATION: synthetic construct
US-10-059-888-26

Query Match 71.1%; Score 12.8; DB 14; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGTGGTGGG 18
||||| |||||
DB 1 GGAGGGGGGGGGGG 16

RESULT 13

US-10-181-846-35
; Sequence 35, Application US/10181846
; Publication No. US20030083297A1
; GENERAL INFORMATION:

; APPLICANT: Nicholas M. Dean
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF DAXX EXPRESSION
; FILE REFERENCE: RTSP-0363
; CURRENT APPLICATION NUMBER: US/10/181,846
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: PCT/US01/01416
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 09/490,692
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-181-846-35

Query Match 71.1%; Score 12.8; DB 14; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGGAGGGGTGGTGG 16
||||| |||||
DB 3 TTGGAGGTGGTGGCG 18

RESULT 14

US-09-988-115A-3/c
; Sequence 3, Application US/09988115A
; Publication No. US20030037347A1
; GENERAL INFORMATION:
; APPLICANT: Robl, James M.
; APPLICANT: Goldsby, Richard A.
; APPLICANT: Ferguson, Stacy E.
; APPLICANT: Kurogiwa, Yoshima
; APPLICANT: Tomizuka, Kazuma
; APPLICANT: Ishida, Isao
; TITLE OF INVENTION: Expression of Xenogenous (Human)
; TITLE OF INVENTION: Immunoglobulins in Cloned, Transgenic Ungulates
; FILE REFERENCE: 50195/008003
; CURRENT APPLICATION NUMBER: US/09/988,115A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,625
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: US 60/256,458
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/714,185
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/166,410
; PRIOR FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-09-988-115A-3

Query Match 71.1%; Score 12.8; DB 11; Length 22;
Best Local Similarity 87.5%; Pred. No. 2.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGGAGGGGTGGTGG 16
||||| |||||
DB 21 TTGGAGGTGGTGGCG 6

RESULT 15

US-09-988-115A-13/c

```
; Sequence 13, Application US/09988115A
; Publication No. US20030037347A1
; GENERAL INFORMATION:
; APPLICANT: Robt. James M.
; APPLICANT: Goldsby, Richard A.
; APPLICANT: Ferguson, Stacy E.
; APPLICANT: Kuroiwa, Yoshima
; APPLICANT: Tomizuka, Kazuma
; APPLICANT: Ishida, Isao
; TITLE OF INVENTION: Expression of Xenogenous (Human)
; IMMUNOGLOBULINS IN CLONED, TRANSGENIC UNGULATES
; FILE REFERENCE: 50195/08003
; CURRENT APPLICATION NUMBER: US/09/988,115A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,625
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: US 60/256,458
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/714,185
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/166,410
; PRIOR FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-09-988-115A-13
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Query Match      71.1%; Score 12.8; DB 11; Length 22;
Best Local Similarity 87.5%; Pred. No. 2.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy      1 TTGAGGGGGTGGTGG 16
          |||||
Db      21 TTGAGGGTGGTGG 6
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Search completed: October 27, 2003, 19:00:52
Job time : 387.943 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:34 ; Search time 41.3143 Seconds
(without alignments)
192.304 Million cell updates/sec

Title: US-09-331-204A-4

Perfect score: 18
Sequence: 1 ttggagggggtggtgggg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 376294

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*
1: /cgn2_6/prodata/1/ina/5A_COMB.seq*
2: /cgn2_6/prodata/1/ina/5B_COMB.seq*
3: /cgn2_6/prodata/1/ina/6A_COMB.seq*
4: /cgn2_6/prodata/1/ina/6B_COMB.seq*
5: /cgn2_6/prodata/1/ina/PCTUS_COMB.seq*
6: /cgn2_6/prodata/1/ina/backfiles1.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	2	US-08-529-878B-3
2	18	100.0	18	2	US-08-529-878B-44
3	18	100.0	21	2	US-08-529-878B-4
4	18	100.0	21	2	US-08-529-878B-45
5	13.4	74.4	20	2	US-08-476-712-2
6	13.4	74.4	20	4	US-09-411-291-2
7	12.8	71.1	17	4	US-09-495-140-26
8	12.8	71.1	18	3	US-09-017-974-57
9	12.8	71.1	18	4	US-08-682-255A-57
10	12.8	71.1	18	4	US-09-429-130-57
11	12.8	71.1	20	3	US-09-490-692-35
12	12.8	71.1	21	2	US-08-632-575B-19
13	12.8	71.1	21	4	US-09-199-542B-19
14	12.2	67.8	17	3	US-09-809-713-3
15	12.2	67.8	18	1	US-08-013-801-4
16	12.2	67.8	18	1	US-08-072-063-13
17	12.2	67.8	18	1	US-08-312-132-4
18	12.2	67.8	18	1	US-08-064-693-13
19	12.2	67.8	18	1	US-08-430-417-4
20	12.2	67.8	18	1	US-08-470-366-4
21	12.2	67.8	18	1	US-08-466-822-4
22	12.2	67.8	18	2	US-08-704-504-4
23	12.2	67.8	18	3	US-08-885-366-13
24	12.2	67.8	18	3	US-09-323-342-4
25	12.2	67.8	18	4	US-09-425-034A-4
26	12.2	67.8	18	5	PCT-US93-04754-13
27	12.2	67.8	18	5	PCT-US94-01235-4

28 12.2 67.8 18 5 PCT-US95-03125-4
c 29 12.2 67.8 19 1 US-08-486-913-2
c 30 12.2 67.8 19 2 US-08-486-535-2
c 31 12.2 67.8 19 2 US-08-300-484-2
c 32 12.2 67.8 19 3 US-08-486-885-2
c 33 12.2 67.8 19 3 US-08-486-536-2
c 34 12.2 67.8 19 3 PCT-US95-11234-2
c 35 12.2 67.8 19 5 US-08-486-913-3
c 36 12.2 67.8 20 1 US-08-486-535-3
c 37 12.2 67.8 20 2 US-08-300-484-3
c 38 12.2 67.8 20 2 US-08-830-980-56
c 39 12.2 67.8 20 3 US-08-830-979-56
c 40 12.2 67.8 20 3 US-08-032-894-56
c 41 12.2 67.8 20 3 US-08-486-885-3
c 42 12.2 67.8 20 3 US-08-031-626-56
c 43 12.2 67.8 20 3 US-08-486-536-3
c 44 12.2 67.8 20 3 US-09-487-368A-174
c 45 12.2 67.8 20 3 US-09-487-368A-174

ALIGNMENTS

RESULT 1
US-08-529-878B-3
; Sequence 3, Application US/08529878B
; Patent No. 5932556
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Crockett & Fish
; STREET: 3000 S. Augusta Court
; CITY: La Habra
; STATE: California
; COUNTRY: United States of America
; ZIP: 90631

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/529,878B
; FILING DATE: 13-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Fish, Robert D.
; REGISTRATION NUMBER: 33,890
; REFERENCE/DOCKET NUMBER: 213/003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-525-3433
; TELEFAX: 714-525-3303
; TELEX:

INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-529-878B-3

Query Match 100.0%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGAGGGGGTGTGGGG 18
DB 1 TTGGAGGGGGTGTGGGG 18

Best Local Similarity 100.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGTGGTGGG 18
Db 4 TTGGAGGGGGTGGTGGG 21

RESULT 5

US-08-476-712-2
; Sequence 2, Application US/08476712
; Patent No. 5962426
; GENERAL INFORMATION:
; APPLICANT: Glazer, Peter, M.
; TITLE OF INVENTION: Triple-Helix Forming Oligonucleotides for
; TITLE OF INVENTION: Targeted Mutagenesis
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,712
; FILING DATE: 7-JUNE-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: YU114
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-873-8794
; TELEFAX: (404)-873-8795
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-476-712-2

Query Match 74.4%; Score 13.4; DB 2; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGGGGTGGTGGG 17
Db 6 GGGGGGGTGGTGGG 20

RESULT 6

US-09-411-291-2
; Sequence 2, Application US/09411291
; Patent No. 6303376
; GENERAL INFORMATION:
; APPLICANT: Glazer, Peter, M.
; TITLE OF INVENTION: Triple-Helix Forming Oligonucleotides for
; TITLE OF INVENTION: Targeted Mutagenesis
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta

Query Match 71.1%; Score 12.8; DB 4; Length 17;
Best Local Similarity 87.5%; Pred. No. 3e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

STATE: GA
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/411,291
FILING DATE: 04-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,712
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: YU114
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-411-291-2

Query Match 74.4%; Score 13.4; DB 4; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGGGGTGGTGGG 17
Db 6 GGGGGGGTGGTGGG 20

RESULT 7

US-09-495-140-26
; Sequence 26, Application US/09495140
; Patent No. 6376182
; GENERAL INFORMATION:
; APPLICANT: CHAO, JULIE
; APPLICANT: CHAO, JULIE
; APPLICANT: SONG, QING
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING
; TITLE OF INVENTION: TISSUE KALLIKREIN GENE PROMOTER POLYMORPHISMS WITH TREATMENT
; TITLE OF INVENTION: OF ESSENTIAL HYPERTENSION
; FILE REFERENCE: 19113.0081
; CURRENT APPLICATION NUMBER: US/09/495,140
; CURRENT FILING DATE: 2000-01-31
; EARLIER APPLICATION NUMBER: 09/389,566
; EARLIER FILING DATE: 1999-09-03
; EARLIER APPLICATION NUMBER: 08/856,141
; EARLIER FILING DATE: 1997-05-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence./No. 6376182e =
; OTHER INFORMATION: synthetic construct
US-09-495-140-26

Query Match 71.1%; Score 12.8; DB 4; Length 17;
Best Local Similarity 87.5%; Pred. No. 3e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGAGGGGGTGGTGGG 18
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 Db 1 GGAGGGGGGGGGGGG 16

RESULT 8

US-09-017-974-57
 ; Sequence 57, Application US/09017974
 ; Patent No. 6288042
 ; GENERAL INFORMATION:
 ; APPLICANT: Rando, Robert F.
 ; APPLICANT: Ojwang, Joshua O.
 ; APPLICANT: Hogan, Michael E.
 ; APPLICANT: Pommier, Eyves
 ; APPLICANT: Mazumder, Abhijit
 ; TITLE OF INVENTION: Anti-Viral Guanosine-Rich
 ; TITLE OF INVENTION: Tetrad Forming Oligonucleotides
 ; NUMBER OF SEQUENCES: 88
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Conley, Rose & Tayon, P.C.
 ; STREET: 600 Travis, Suite 1800
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: U.S.A.
 ; ZIP: 77002-2912
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: MS Word 97 (saved as .txt file)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/017,974
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/037,374
 ; FILING DATE: 04-FEB-97
 ; APPLICATION NUMBER:
 ; FILING DATE: 09-DEC-97
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McDaniel, C. Steven
 ; REGISTRATION NUMBER: 33,962
 ; REFERENCE/DOCKET NUMBER: 1472-06223
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 713/238-8010
 ; TELEFAX: 713/238-8008
 ; INFORMATION FOR SEQ ID NO: 57:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 18 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-09-017-974-57

Query Match 71.1%; Score 12.8; DB 3; Length 18;
 Best Local Similarity 87.5%; Pred. No. 3.1e+03;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGGAGGGGGTGGTGGG 17
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 Db 2 TGGTGGGTGGTGGG 17

RESULT 9

US-08-682-255A-57
 ; Sequence 57, Application US/08682255A
 ; Patent No. 6323185
 ; GENERAL INFORMATION:
 ; APPLICANT: Rando, Robert F.
 ; APPLICANT: Fennewald, Susan
 ; APPLICANT: Zendegui, Joseph G.

; APPLICANT: Ojwang, Joshua O.
 ; APPLICANT: Hogan, Michael E.
 ; APPLICANT: Pommier, Eyves
 ; APPLICANT: Mazumder, Abhijit
 ; TITLE OF INVENTION: Anti-Viral Guanosine-Rich
 ; TITLE OF INVENTION: Oligonucleotides
 ; NUMBER OF SEQUENCES: 87
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Conley, Rose & Tayon, P.C.
 ; STREET: 600 Travis, Suite 1850
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: U.S.A.
 ; ZIP: 77002-2912
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: MS Windows 95
 ; SOFTWARE: MS Word 97 (saved as .txt file)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/682,255A
 ; FILING DATE: 17-JULY-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/535,168
 ; FILING DATE: 23-OCT-95
 ; APPLICATION NUMBER: 60/001,505
 ; FILING DATE: 19-JULY-95
 ; APPLICATION NUMBER: 60/014,007
 ; FILING DATE: 25-MARCH-96
 ; APPLICATION NUMBER: 60/013,688
 ; FILING DATE: 19-MARCH-96
 ; APPLICATION NUMBER: 60/015,714
 ; FILING DATE: 17-APRIL-96
 ; APPLICATION NUMBER: 60/016,271
 ; FILING DATE: 23-APRIL-96
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McDaniel, C. Steven
 ; REGISTRATION NUMBER: 33,962
 ; REFERENCE/DOCKET NUMBER: 1472-06214
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 713/238-8010
 ; TELEFAX: 713/238-8008
 ; INFORMATION FOR SEQ ID NO: 57:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 18 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-682-255A-57

Query Match 71.1%; Score 12.8; DB 4; Length 18;
 Best Local Similarity 87.5%; Pred. No. 3.1e+03;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGGAGGGGGTGGTGGG 17
 |||||
 Db 2 TGGTGGGTGGTGGG 17

RESULT 10

US-09-429-130-57
 ; Sequence 57, Application US/09429130
 ; Patent No. 6355785
 ; GENERAL INFORMATION:
 ; APPLICANT: Rando, Robert F.
 ; APPLICANT: Fennewald, Susan
 ; APPLICANT: Zendegui, Joseph G.
 ; APPLICANT: Ojwang, Joshua O.
 ; APPLICANT: Hogan, Michael E.
 ; APPLICANT: Pommier, Eyves
 ; APPLICANT: Mazumder, Abhijit

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/ 60/015.714
/ TITLE OF INVENTION: Anti-Viral Guanosine-Rich
/ Oligonucleotides
/ NUMBER OF SEQUENCES: 87
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Conley, Rose & Tayon, P.C.
/ STREET: 600 Travis, Suite 1850
/ CITY: Houston
/ STATE: Texas
/ COUNTRY: U.S.A.
/ ZIP: 77002-2912
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: MS Windows 95
/ SOFTWARE: MS Word 97 (saved as .txt file)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/429,130
/ FILING DATE: 28-Oct-1999
/ CLASSIFICATION: <Unknown>
/ 19-JULY-95
/ 25-MARCH-96
/ 19-MARCH-96
/ 17-APRIL-96
/ 23-APRIL-96
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/682,255
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: 60/001,505
/ FILING DATE: 19-JULY-95
/ APPLICATION NUMBER: 60/014,007
/ FILING DATE: 25-MARCH-96
/ APPLICATION NUMBER: 60/013,688
/ FILING DATE: 19-MARCH-96
/ APPLICATION NUMBER: 60/016,271
/ FILING DATE: 17-APRIL-96
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McDaniel, C. Steven
/ REGISTRATION NUMBER: 33,962
/ REFERENCE/DOCKET NUMBER: 1472-06214
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 713/238-8010
/ TELEFAX: 713/238-8008
/ INFORMATION FOR SEQ ID NO: 57:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-09-429-130-57
Query Match 71.1%; Score 12.8; DB 4; Length 18;
Best Local Similarity 87.5%; Pred. No. 3.1e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 2 TGGAGGGGGTGGTGG 17
Db 2 TGGTGGGTGGTGGG 17

RESULT 11
US-09-490-692-35
/ Sequence 35, Application US/09490692
/ Patent No. 6180353
/ GENERAL INFORMATION:
/ APPLICANT: Nicholas M. Dean
/ APPLICANT: Lex M. Cowert
/ TITLE OF INVENTION: ANTISENSE MODULATION OF DAXX EXPRESSION
/ FILE REFERENCE: RTS-0120
/ CURRENT APPLICATION NUMBER: US/09/490,692
/ CURRENT FILING DATE: 2000-01-24
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/ NUMBER OF SEQ ID NOS: 176
/ SEQ ID NO 35
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Antisense Oligonucleotide
US-09-490-692-35
Query Match 71.1%; Score 12.8; DB 3; Length 20;
Best Local Similarity 87.5%; Pred. No. 3.1e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 1 TTGGAGGGGGTGGTGG 16
Db 3 TTGGAGGTGGTGGCGG 18

RESULT 12
US-08-632-575B-19
/ Sequence 19, Application US/08632575B
/ Patent No. 5843660
/ GENERAL INFORMATION:
/ APPLICANT: Schumm, James W.
/ TITLE OF INVENTION: Multiplex Amplification of
/ TITLE OF INVENTION: Short Tandem Repeat Loci
/ NUMBER OF SEQUENCES: 61
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Promega Corporation
/ STREET: 2800 Woods Hollow Road
/ CITY: Madison
/ STATE: Wisconsin
/ COUNTRY: U.S.A.
/ ZIP: 53711-5399
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
/ COMPUTER: IBM compatible PC
/ OPERATING SYSTEM: DOS, version 6.0
/ SOFTWARE: Wordperfect 5.1 (DOS text format)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/632,575B
/ FILING DATE: 04/15/96
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/316,544
/ FILING DATE: 09/30/94
/ INFORMATION FOR SEQ ID NO: 19:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 21
/ TYPE: Nucleic Acid
/ STRANDEDNESS: Single
/ TOPOLOGY: Linear
/ POSITION IN GENOME:
/ MAP POSITION: D14S562
US-08-632-575B-19
Query Match 71.1%; Score 12.8; DB 2; Length 21;
Best Local Similarity 87.5%; Pred. No. 3.1e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 1 TTGGAGGGGGTGGTGG 16
Db 2 TTGGAGGTGGTGGTGG 17

RESULT 13
US-09-199-542B-19
/ Sequence 19, Application US/09199542B
/ Patent No. 6479235
/ GENERAL INFORMATION:
/ APPLICANT: Schumm, James W.
/ APPLICANT: Sprecher, Cynthia J.
/ TITLE OF INVENTION: Multiplex Amplification of Short Tandem Repeat Loci
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; FILE REFERENCE: 16026/9212
; CURRENT APPLICATION NUMBER: US/09/199,542B
; CURRENT FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: US 08/316,544
; PRIOR FILING DATE: 1994-09-30
; PRIOR APPLICATION NUMBER: US 08/632,575
; PRIOR FILING DATE: 1996-04-15
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: word97 (converted to DOS text format)
; SEQ ID NO 19
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapien
; LOCATION: D14S562
US-09-199-542B-19

Query Match          71.1%; Score 12.8; DB 4; Length 21;
Best Local Similarity 87.5%; Pred.No.3.1e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  1 TTGGAGGGGGTGGTGG 16
Db  2 TTGGAGGGGGTGGTGG 17

RESULT 14
US-09-809-713-3
; Sequence 3, Application US/09809713
; Patent No. 6428564
; GENERAL INFORMATION:
; APPLICANT: Shuber, Anthony
; TITLE OF INVENTION: Method For Alteration Detection
; FILE REFERENCE: EXT-047
; CURRENT APPLICATION NUMBER: US/09/809,713
; CURRENT FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: probe upstream of the 1450 point mutation region
US-09-809-713-3

Query Match          67.8%; Score 12.2; DB 4; Length 17;
Best Local Similarity 82.4%; Pred.No.5.3e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2 TGGAGGGGGTGGTGGG 18
Db  1 TTGAGGAGGTGGTGGAG 17

RESULT 15
US-08-013-801-4
; Sequence 4, Application US/08013801
; Patent No. 5420019
; GENERAL INFORMATION:
; APPLICANT: Theofan, Georgia
; APPLICANT: Horwitz, Arnold
; APPLICANT: Burke, David
; APPLICANT: Baltain, Manik
; APPLICANT: Grinna, Lynn S
; TITLE OF INVENTION: Stable Bactericidal/Permeability-
; TITLE OF INVENTION: Increasing Protein Products and Pharmaceutical
; TITLE OF INVENTION: Compositions Containing the Same
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza
; CITY: Chicago
```

```
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/013,801
; FILING DATE: 02 FEB 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 27129/30911
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/346-5750
; TELEFAX: 312/346-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-013-801-4

Query Match          67.8%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred.No.5.3e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2 TGGAGGGGGTGGTGGG 18
Db  2 TGGAGGGGGTGGTGGT 18

Search completed: October 27, 2003, 14:03:33
Job time : 42.3143 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:29 ; Search time 1581.77 Seconds
(without alignments)
276.576 Million cell updates/sec

Title: US-09-331-204A-4
Perfect score: 18
Sequence: 1 ttggagggggtggtggg 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 11152

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estm:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_val:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13.2	73.3	21	28	AZ468862
C 2	12.8	71.1	19	28	AZ760597
C 3	12.8	71.1	20	28	AZ512326
C 4	12.8	71.1	20	28	AZ645269

C 5	12.8	71.1	20	28	AZ659755
C 6	12.8	71.1	20	28	AZ969440
C 7	12.8	71.1	21	28	AZ583408
C 8	12.8	71.1	21	28	AZ774703
C 9	12.8	71.1	21	28	AZ969578
C 10	12.8	71.1	22	28	AZ307952
C 11	12.8	71.1	22	28	AZ645874
C 12	12.8	71.1	22	28	AZ769521
C 13	12.8	71.1	22	28	AZ871408
C 14	12.8	71.1	18	13	BQ901245
C 15	12.2	67.8	19	9	A1251781
C 16	12.2	67.8	19	28	AZ315293
C 17	12.2	67.8	20	28	AZ622226
C 18	12.2	67.8	20	28	AZ666896
C 19	12.2	67.8	21	28	AZ856540
C 20	12.2	67.8	22	9	A1568336
C 21	12.2	67.8	22	28	AZ766712
C 22	12.2	67.8	22	28	AZ876923
C 23	11.8	65.6	19	9	A1364573
C 24	11.8	65.6	21	28	AZ476392
C 25	11.8	65.6	21	28	AZ512534
C 26	11.8	65.6	22	9	A1183338
C 27	11.8	65.6	22	9	A1434548
C 28	11.8	65.6	22	9	A1582080
C 29	11.8	65.6	22	9	A1735392
C 30	11.8	65.6	22	13	BQ585098
C 31	11.8	65.6	22	28	AZ331988
C 32	11.8	65.6	22	28	AZ607348
C 33	11.6	64.4	20	28	AZ391085
C 34	11.6	64.4	20	28	AZ430735
C 35	11.6	64.4	20	28	AZ845320
C 36	11.6	64.4	21	28	AZ995847
C 37	11.6	64.4	22	14	D21051
C 38	11.6	64.4	22	28	AZ792883
C 39	11.4	63.3	15	9	A1590540
C 40	11.4	63.3	15	9	A1807936
C 41	11.4	63.3	19	28	AZ369361
C 42	11.4	63.3	19	28	AZ381798
C 43	11.4	63.3	19	28	AZ447936
C 44	11.4	63.3	19	28	AZ780591
C 45	11.4	63.3	20	28	AZ405596

ALIGNMENTS

RESULT 1
A2468862
LOCUS
DEFINITION 1M0282004F Mouse 10kb plasmid UGCLM library Mus musculus genomic
clone UGCLM0282004 F, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AZ468862 21 bp DNA linear GSS 04-OCT-2000
1M0282004F Mouse 10kb plasmid UGCLM library Mus musculus genomic
clone UGCLM0282004 F, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AZ468862 21 bp DNA linear GSS 04-OCT-2000
1M0282004F Mouse 10kb plasmid UGCLM library Mus musculus genomic
clone UGCLM0282004 F, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0282 row: 0 column: 04
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers

FEATURES

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1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0282O04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
0 a 1 c 15 g 5 t

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BASE COUNT

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ORIGIN
Query Match 73.3%; Score 13.2; DB 28; Length 21;
Best Local Similarity 83.3%; Pred. No. 5.6e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 TTGAGGGGGTGGTGGGG 18
    ||||| ||||| |||||
Db 1 TTGAGGGGGTGGTGGGG 18

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RESULT 2

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AZ760597 19 bp DNA linear GSS 16-FEB-2001
LOCUS
DEFINITION
clone UUGC1M0554N21 F, genomic survey sequence.

```

```

ACCESSION
AZ760597
VERSION
AZ760597.1 GI:12868613
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)

```

ORGANISM

```

Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606

```

TITLE

```

JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606

```

Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0554 row: N column: 21
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers

FEATURES

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1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0554N21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
0 a 18 c 0 g 1 t

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BASE COUNT

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ORIGIN
Query Match 71.1%; Score 12.8; DB 28; Length 19;
Best Local Similarity 87.5%; Pred. No. 7.6e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 3 GCAGGGGGTGGTGGGG 18
    ||||| ||||| |||||
Db 18 GCAGGGGGTGGTGGGG 3

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RESULT 3

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AZ512326 20 bp DNA linear GSS 05-OCT-2000
LOCUS
DEFINITION
clone UUGC1M0357I18 R, genomic survey sequence.

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ACCESSION
AZ512326
VERSION
AZ512326.1 GI:10693642
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)

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ORGANISM

```

Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

```

TITLE

```

JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

```

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0357 row: 1 column: 18
 Seq primer: CACACAGGAACACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers

FEATURES

source

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    /mol_type="genomic DNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC1M0510B18"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
    /clone_lib="Mouse 10kb plasmid UUGC1M library"
    /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
  
```

BASE COUNT
 ORIGIN

0 a 18 c 2 t

Query Match 71.1%; Score 12.8; DB 28; Length 20;

Best Local Similarity 87.5%; Pred. No. 7.6e+05; Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGAGGGGGTGTGGGG 18

Db 18 GGAGGGGGGGGGGGG 3

RESULT 4

AZ645269/c

LOCUS

DEFINITION 1M0510B10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0510B10 R, genomic survey sequence.

ACCESSION

AZ645269

VERSION

GSS.

SOURCE

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0510 row: B column: 10

Seq primer: CACACAGGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

FEATURES

source

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1..20
    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC1M0510B10"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
    /clone_lib="Mouse 10kb plasmid UUGC1M library"
    /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
  
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BASE COUNT 0 a 19 c 0 g 1 t

Query Match 71.1%; Score 12.8; DB 28; Length 20;

Best Local Similarity 87.5%; Pred. No. 7.6e+05; Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGAGGGGGTGTGGGG 18

Db 17 GGAGGGGGGGGGGGG 2

RESULT 5

AZ659755/c

LOCUS

DEFINITION 1M053722F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M053722 F, genomic survey sequence.

ACCESSION

AZ659755

VERSION

GSS.

SOURCE

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0537 row: F column: 22
 Seq primer: CGTGTAAACGACGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 20.

FEATURES

Location/Qualifiers

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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="JUGC1M0537F22"
 /sex="Male"
 /lab_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 18 c 0 g 2 t
 ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 20;
 Best Local Similarity 87.5%; Pred. No. 7.6e+05;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGTGTGGGG 18
 |||||
 Db 20 GGAGGGGGGGGGGGG 5

RESULT 6
 AZ969440/c 20 bp DNA linear GSS 27-APR-2001
 LOCUS 2M0242012F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
 DEFINITION clone UUGC2M0242012 F, genomic survey sequence.

ACCESSION AZ969440
 VERSION AZ969440.1 GI:13840667
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1. (bases 1 to 20)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center

University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0242 row: O column: 12
 Seq primer: CGTGTAAACGACGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 20.

FEATURES

Location/Qualifiers

1..20
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0242012"
 /sex="Female"
 /lab_hosts="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC2M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 19 c 0 g 1 t
 ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 20;
 Best Local Similarity 87.5%; Pred. No. 7.6e+05;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGTGTGGGG 18
 |||||
 Db 16 GGAGGGGGGGGGGGG 1

RESULT 7
 AZ583408/c 21 bp DNA linear GSS 13-DEC-2000

LOCUS 1M0378N23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0378N23 F, genomic survey sequence.

ACCESSION AZ583408
 VERSION AZ583408.1 GI:11703261
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1. (bases 1 to 21)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished
 COMMENT Contact: Robert B. Weiss

University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0378 row: N column: 23
 Seq primer: CGTTGTAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 21.

FEATURES

1..21
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0378N23"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 20 c 0 g 1 t
 ORIGIN
 Query Match 71.1%; Score 12.8; DB 28; Length 21;
 Best Local Similarity 87.5%; Pred. No. 7.5e+05;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 GGAGGGGGTGGTGGG 18
 Db 18 GGAGGGGGGGGGGGG 3

RESULT 8
 AZ774703/c
 LOCUS
 DEFINITION 2H0004G14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 Clone UUGC2M0004G14 F, genomic survey sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE
 JOURNAL

Unpublished
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

COMMENT

Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0004 row: G column: 14
 Seq primer: CGTTGTAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 21.

FEATURES

1..21
 Location/Qualifiers
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0004G14"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 2 a 19 c 0 g 0 t
 ORIGIN
 Query Match 71.1%; Score 12.8; DB 28; Length 21;
 Best Local Similarity 87.5%; Pred. No. 7.5e+05;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 GGAGGGGGTGGTGGG 18
 Db 21 GGAGGGGGGGGGGGG 6

RESULT 9
 AZ969578/c
 LOCUS
 DEFINITION 2M0242G20F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
 Clone UUGC2M0242G20 F, genomic survey sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE
 JOURNAL

Unpublished
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
COMMENT

Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112 USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: rdunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0242 row: G column: 20
Seq primer: CGTTGTAACACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers

FEATURES
source

1..21
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGC2M0242G20"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|473114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN
1 a 18 c 0 g 2 c

Query Match 71.1%; Score 12.8; DB 28; Length 21;
Best Local Similarity 87.5%; Pred. No. 7.5e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGTGTGGGG 18
|||||
Db 21 GGAGGGGGAGTGGGG 6

RESULT 10
AZ307952

LOCUS
DEFINITION
IM0010L24F Mouse 10kb plasmid UGC1M library Mus musculus genomic clone UGC1M0010L24 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AZ307952.1 GI:10347459

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL
COMMENT

plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: rdunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0010 row: L column: 24
Seq primer: CGTTGTAACACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES
source

1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGC1M0010L24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|473114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN
5 a 0 c 14 g 3 t

Query Match 71.1%; Score 12.8; DB 28; Length 22;
Best Local Similarity 87.5%; Pred. No. 7.5e-05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGTGTGGGG 19
|||||
Db 4 GGAGGGGGGTGGGG 19

RESULT 11
AZ645874/c

LOCUS
DEFINITION
IM0511C07R Mouse 10kb plasmid UGC1M library Mus musculus genomic clone UGC1M0511C07 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AZ645874.1 GI:11775791

Mus musculus (house mouse)

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
Plasmid inserts
JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0511 row: C column: 07
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.

FEATURES

source

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1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0511C07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWP42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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BASE COUNT
ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 22;

Best Local Similarity 87.5%; Pred. No. 7.5e+05;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGTGGTGGGG 18

DB 17 GGAGGGGGGGGGGGG 2

RESULT 12

AZ769521/c
LOCUS

DEFINITION 1M0570018F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0570018 F, genomic survey sequence.

ACCESSION AZ769521

VERSION AZ769521.1

KEYWORDS GI:12889741

SOURCE GSS.

ORGANISM Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 22)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
Plasmid inserts
JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0570 row: O column: 18
Seq primer: CGTGTAAACAGCGCCAGT
Class: plasmid ends
High quality sequence stop: 22.

FEATURES

source

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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWP42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

BASE COUNT
ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 22;

Best Local Similarity 87.5%; Pred. No. 7.5e+05;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGTGGTGGGG 18

DB 21 GGAGGGGGGGTGGGGG 6

RESULT 13

AZ871408/c

LOCUS

DEFINITION 2M0184E16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0184E16 F, genomic survey sequence.

ACCESSION AZ871408

VERSION AZ871408.1

KEYWORDS GI:13077580

SOURCE GSS.

ORGANISM Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 22)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: cdunagene@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0184 row: E column: 16
 Seq primer: CGTTGTAAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 22.

FEATURES

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 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UNG2M0184E16"
 /sex="Male"
 /lab_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGCIM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 0 a 21 c 0 g 1 t
 ORIGIN
 Query Match 71.1%; Score 12.8; DS 28; Length 22;
 Best Local Similarity 87.5%; Pred. No. 7.5e+05;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGAGGGGGTGTGGGG 18
 Db 16 GGAGGGGGGGGGGGG 1

RESULT 14

BQ901245 18 bp mRNA linear EST 19-AUG-2002
 hasp002xj21f Heterobasidion annosum - Scots pine infection stage
 subtraction cDNA library (hasp) Pinus sylvestris/Heterobasidion
 annosum cDNA clone hasp002xj21f, mRNA sequence.

ACCESSION BQ901245.1 GI:22300029
 VERSION BQ901245
 KEYWORDS EST.
 SOURCE Pinus sylvestris/Heterobasidion annosum
 ORGANISM Pinus sylvestris/Heterobasidion annosum
 Eukaryota; mixed EST libraries.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Asiegbu, F.O., Nahalkova, J. and Dean, R.A.

TITLE

JOURNAL COMMENT

Selected Expressed sequence tags of cDNA clones from the
 interaction of the root rot fungus (Heterobasidion annosum) with
 seedling roots of Scots pine (Pinus sylvestris)
 Unpublished
 Contact: Fred O. Asiegbu
 Dept. of Forest Mycology & Pathology
 Swedish University of Agriculture, Box 7026, S-750 07, Uppsala,
 Sweden
 Tel: +46 18 67 15 98
 Fax: +46 18 30 92 45
 Email: Fred.Asiegbu@mykopat.slu.se
 Seq primer: T7 primer.
 Location/Qualifiers
 1..18
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 /mol_type="mRNA"
 /db_xref="taxon:169015"
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 /dev_stage="Seedling roots of scots pine were infected for
 6 days with H. annosum"
 /clone_lib="Heterobasidion annosum - Scots pine infection
 stage subtraction cDNA library (hasp)"
 /note="Vector: pT-Adv; Site 1: EcoRI; The subtractive
 hybridization cDNA library was constructed from scots
 pine roots infected for 6-days with mycelia of
 Heterobasidion annosum (FPS)."
 Heterobasidion annosum (FPS)."
 0 a 0 c 17 g 1 t

FEATURES

source

BASE COUNT 0 a 0 c 17 g 1 t
 ORIGIN
 Query Match 67.8%; Score 12.2; DS 13; Length 18;
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 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TCGAGGGGGTGTGGGG 18
 Db 2 TCGGGGGGGGGGGGG 18

RESULT 15

AL251781/c

LOCUS

AL251781 19 bp mRNA linear EST 05-NOV-1998
 qu76g01.x1 NCI CGAP Brn35 Homo sapiens cDNA clone IMAGE:1978032.3.
 similar to TR:Q39949 Q39949 HYDROXYPROLINE-RICH PROTEIN. 1; mRNA
 sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL COMMENT

FEATURES

source

AL251781.1 GI:3948310
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 19)
 NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute / National Institute of Neurological
 Disorders and Stroke, Brain Tumor Genome Anatomy Project
 (CGAP/BrGAP), Tumor Gene Index
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 unknown library type
 Trace considered overall poor quality
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1.
 Location/Qualifiers
 1..19
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
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 /lab_host="DH10B"
 /clone_lib="NCI CGAP Brn35"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: SalI;

Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.33 kb. Tumor types include:
 meningioma, oligodendroglioma, astrocytoma (grade II),
 medulloblastoma, astrocytoma (grade IV). Life Technologies
 catalog #: 11544-012"

BASE COUNT 4 a 14 c 0 g 1 t
 ORIGIN

Query Match 67.8%; Score 12.2; DB 9; Length 19;
 Best Local Similarity 82.4%; Pred. No. 1.2e+06;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTGGAGGGGGTGGTGGG 17
 |||||
 Db 17 TTGGGGGGGAGGGGG 1

Search completed: October 27, 2003, 13:59:22
 Job time : 1585.77 secs


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FEATURES
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  Best Local Similarity 100.0%; Pred. No. 4.1e+03;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGAGGGGGTGGTGGG 18
Db 1 TTGAGGGGGTGGTGGG 18

RESULT 2
AX023427/c
LOCUS AX023427 18 bp DNA linear PAT 15-SEP-2000
DEFINITION Sequence 42 from Patent WO0014217.
ACCESSION AX023427
VERSION AX023427.1 GI:10183827
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
  artificial sequences.
REFERENCE
  1 Lipford,G.B., Heeg,K. and Wagner,H.
  G-motif oligonucleotides and uses thereof
  Patent: WO 0014217-A 42 16-MAR-2000;
  LIPFORD GRAYSON B (DE) ; HEEG KLAUS (DE) ; WAGNER HERMANN (DE) ;
  CPG IMMUNOPHARMACEUTICALS GMBH (DE)
  Location/Qualifiers
    1..18
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    /note="synthetic, no natural origin"
BASE COUNT
  4 a 13 c 0 g 1 t
ORIGIN

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  Best Local Similarity 100.0%; Pred. No. 4.1e+03;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGAGGGGGTGGTGGG 18
Db 18 TTGAGGGGGTGGTGGG 1

RESULT 3
AR078333
LOCUS AR078333 20 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 2 from patent US 5962426.
ACCESSION AR078333
VERSION AR078333.1 GI:10005079
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
  Unclassified.
  1 (bases 1 to 20)
REFERENCE
  1 Glazer,P.M.
  Triple-helix forming oligonucleotides for targeted mutagenesis
  Patent: US 5962426-A 2 05-OCT-1999;
  JOURNAL
  FEATURES
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        1..20
        /organism="unknown"
BASE COUNT
  3 a 0 c 15 g 2 t
ORIGIN

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  Best Local Similarity 93.3%; Pred. No. 3.4e+05;
  Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGAGGGGGTGGTGGG 17
Db 6 GGAGGGGGTGGTGGG 20

RESULT 4
AR173053
LOCUS AR173053 20 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 2 from patent US 6303376.
ACCESSION AR173053
VERSION AR173053.1 GI:17912544
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
  Unclassified.
  1 (bases 1 to 20)
REFERENCE
  1 Glazer,P.M.
  Methods of targeted mutagenesis using triple-helix forming
  oligonucleotides
  Patent: US 6303376-A 2 16-OCT-2001;
  JOURNAL
  FEATURES
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        1..20
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  Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGAGGGGGTGGTGGG 17
Db 6 GGAGGGGGTGGTGGG 20

RESULT 5
AX384817
LOCUS AX384817 21 bp DNA linear PAT 19-MAR-2002
DEFINITION Sequence 17 from Patent WO210452.
ACCESSION AX384817
VERSION AX384817.1 GI:19577951
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
  artificial sequences.
REFERENCE
  1 Chang,C.
  Methods and compositions for predicting prostate cancer
  Patent: WO 0210452-A 17 07-FEB-2002;
  JOURNAL
  FEATURES
    source
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  Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGGAGGGGGTGGTGG 16
Db 6 TGGAGGGGGTGGTGG 20

RESULT 6

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AR168831
LOCUS 18 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 57 from patent US 6288042.
ACCESSION AR168831
VERSION AR168831.1 GI:17904956
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 18)
Rando,R.F., Ojwang,J.O., Hogan,M.E., Wallace,T.L. and Cossum,P.A.
TITLE Anti-viral guanosine-rich tetrad forming oligonucleotides
JOURNAL Patent: US 6288042-A 57 11-SEP-2001;
FEATURES
1. .18
Location/Qualifiers
source /organism="unknown"
BASE COUNT 0 a 0 c 12 g 6 t
ORIGIN
Query Match 71.1%; Score 12.8; DB 6; Length 18;
Best Local Similarity 87.5%; Pred. No. 6.2e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TGGAGGGGGTGGTGGG 17
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Db 2 TGGTGGGTGGTGGG 17
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RESULT 7
LOCUS 18 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 57 from patent US 6355785.
ACCESSION AR200300
VERSION AR200300.1 GI:20250374
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 18)
Rando,R.F., Fennekald,S., Zendegei,J.G., Ojwang,J.O., Hogan,M.E.,
Pommier,Y. and Mazunder,A.
TITLE Guanosine-rich oligonucleotide integrase inhibitors
JOURNAL Patent: US 6355785-A 57 12-MAR-2002;
FEATURES
1. .18
Location/Qualifiers
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BASE COUNT 0 a 0 c 12 g 6 t
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Query Match 71.1%; Score 12.8; DB 6; Length 18;
Best Local Similarity 87.5%; Pred. No. 6.2e+05;
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QY 2 TGGAGGGGGTGGTGGG 17
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Db 2 TGGTGGGTGGTGGG 17
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RESULT 8
LOCUS 18 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 57 from patent US 6323185.
ACCESSION AR262431
VERSION AR262431.1 GI:28073862
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 18)
Rando,R.F., Fennekald,S., Zendegei,J.G., Ojwang,J.O. and Hogan,M.E.
TITLE Anti-viral guanosine-rich oligonucleotides and method of treating
JOURNAL Patent: US 6323185-A 57 27-NOV-2001;

FEATURES
source Location/Qualifiers
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BASE COUNT 0 a 0 c 12 g 6 t
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Query Match 71.1%; Score 12.8; DB 6; Length 18;
Best Local Similarity 87.5%; Pred. No. 6.2e+05;
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Db 2 TGGTGGGTGGTGGG 17
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RESULT 9
LOCUS 18 bp DNA linear PAT 29-SEP-1997
DEFINITION linker.
ACCESSION E04543
VERSION E04543.1 GI:2172744
KEYWORDS JP 1993078397-A/18.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
1 (bases 1 to 18)
Yamazaki,C., Takasu,N., Negoro,T. and Agui,H.
TITLE THROMBOCYTIC PROTEIN
JOURNAL Patent: JP 1993078397-A 18 30-MAR-1993;
COMMENT OS Artificial Gene
OC Artificial sequence; Genes.
PN JP 1993078397-A/18
PD 30-MAR-1993
PF 29-JAN-1991 JP 1991029624
PI YAMAZAKI CHIE, TAKASU NAOKO, NEGORO TAKAATSU, AGUI HIDEO PC
C07K13/00,A61K37/24,A61K37/54,C12N1/19,C12N1/21,C12N5/10, PC
C12N9/64.
PC C12N15/58,C12N15/62,C12N15/70,C12N15/81,C12N15/85//C12P21/02,
PC C12N1/21,
PC C12N1/19),(C12P21/02,C12R1:19);
CC strandedness: Single;
CC topology: Linear.
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Location/Qualifiers
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/mol_type="genomic DNA"
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BASE COUNT 3 a 2 c 11 g
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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 TTGAGGGGGTGGTGGG 16
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Db 2 TAGGAGGGGGCGGTGG 17
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RESULT 10
LOCUS 19 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 3 from Patent WO02102824.
ACCESSION AX659401
VERSION AX659401.1 GI:29161631
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
1
Beimfohr,C. and Snaidr,J.
TITLE Method for specific fast detection of relevant bacteria in drinking

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water
Patent: WO 02102824-A 3 27-DEC-2002;
Vermicon AG (DE)
FEATURES
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    Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTGGAGGGGTGGTGG 16
Db 16 TGGAGAGGGTGGTGG 1

RESULT 11
LOCUS AR126606 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 35 from patent US 6180353.
ACCESSION AR126606
VERSION AR126606.1 GI:14113199
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
    1 (bases 1 to 20)
AUTHORS Dean.N.M. and Cowser.L.M.
TITLE Antisense modulation of daxx expression
JOURNAL Patent: US 6180353-A 35 30-JAN-2001;
FEATURES
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            1..20
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    Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTGGAGGGGTGGTGG 16
Db 3 TTGGAGGTGGTGGCGG 18

RESULT 12
LOCUS A20477/c 21 bp DNA linear PAT 11-MAR-1996
DEFINITION oligonucleotide primer for Sry.
ACCESSION A20477
VERSION A20477.1 GI:1566754
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
    1 (bases 1 to 21)
AUTHORS
TITLE SEXE DETERMINING GENE
JOURNAL Patent: WO 9200375-A 4 09-JAN-1992;
FEATURES
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Query Match
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water
Patent: WO 02102824-A 3 27-DEC-2002;
Vermicon AG (DE)
FEATURES
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BASE COUNT
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    Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTGGAGGGGTGGTGG 16
Db 16 TGGAGAGGGTGGTGG 1

RESULT 11
LOCUS AR126606 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 35 from patent US 6180353.
ACCESSION AR126606
VERSION AR126606.1 GI:14113199
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
    1 (bases 1 to 20)
AUTHORS Dean.N.M. and Cowser.L.M.
TITLE Antisense modulation of daxx expression
JOURNAL Patent: US 6180353-A 35 30-JAN-2001;
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    Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTGGAGGGGTGGTGG 16
Db 3 TTGGAGGTGGTGGCGG 18

RESULT 12
LOCUS A20477/c 21 bp DNA linear PAT 11-MAR-1996
DEFINITION oligonucleotide primer for Sry.
ACCESSION A20477
VERSION A20477.1 GI:1566754
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
    1 (bases 1 to 21)
AUTHORS
TITLE SEXE DETERMINING GENE
JOURNAL Patent: WO 9200375-A 4 09-JAN-1992;
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Qy 1 TTGGAGGGGTGGTGG 16
Db 21 TTGGTGGTGGTGGTGG 6

RESULT 13
LOCUS A28676/c 21 bp mRNA linear PAT 04-JUN-1995
DEFINITION dsRNA with central hinge (comp.).
ACCESSION A28676
VERSION A28676.1 GI:1248715
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
    1 (bases 1 to 21)
AUTHORS
TITLE SHORT THERAPEUTIC dsRNA OF DEFINED STRUCTURE
JOURNAL Patent: WO 9014090-A 4 29-NOV-1990;
FEATURES
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Db 19 GGGGGGTGGGGGGG 4

RESULT 14
LOCUS AR061827 21 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 19 from patent US 5843660.
ACCESSION AR061827
VERSION AR061827.1 GI:5989518
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
    1 (bases 1 to 21)
AUTHORS Schumm,J.W., Micka,K.A. and Rabbach,D.R.
TITLE Multiplex amplification of short tandem repeat loci
JOURNAL Patent: US 5843660-A 19 01-DEC-1998;
FEATURES
    Location/Qualifiers
        source
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                /organism="unknown"
BASE COUNT
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Query Match
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    Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTGGAGGGGTGGTGG 16
Db 2 TTGGAGGTGGGTGG 17

RESULT 15
LOCUS AR252818 21 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 19 from patent US 6479235.
ACCESSION AR252818
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VERSION AR252918.1 GI:27301167
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Schumm,J.W. and Sprecher,C.J.
TITLE Multiplex amplification of short tandem repeat loci
JOURNAL Patent: US 6479235-A 19 12-NOV-2002;
FEATURES Location/Qualifiers
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BASE COUNT 3 a 2 c 11 g 5 t
ORIGIN

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Best Local Similarity 87.5%; Pred.No. 6e+05; 2; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTGGAGGGGGTGGTGG 16
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Db 2 TTGGAGGGTGGGGTGG 17
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Job time : 380.114 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:29 ; Search time 162 Seconds
(without alignments)
299,938 Million cell updates/sec

Title: US-09-331-204a-4

Perfect score: 18
Sequence: 1 ttggaggggggtggtggg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

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- 23: /SIDSI/gcgdata/genseq/genseqn-emb1/NA2001B.DAT.*
- 24: /SIDSI/gcgdata/genseq/genseqn-emb1/NA2002.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	18	100.0	18	17 AAT36196	Triplex forming ol
2	18	100.0	18	20 AAX90328	CD28 inhibiting ph
3	18	100.0	18	20 AAX90320	CD28 inhibition ol
4	18	100.0	18	21 AAX99625	Nucleotide sequenc
5	18	100.0	18	21 AAX99650	Nucleotide sequenc
6	18	100.0	21	17 AAT36197	Triplex forming ol
7	18	100.0	21	20 AAX90329	CD28 inhibiting ph
8	18	100.0	21	20 AAX90291	CD28 inhibition ol

9	16.4	91.1	18	17 AAT36243	CD28 expression in
10	16.4	91.1	18	20 AAX90336	CD28 inhibiting ph
11	14.8	82.2	18	17 AAT36242	CD28 expression in
12	14.8	82.2	18	17 AAT36244	CD28 expression in
13	14.8	82.2	18	20 AAX90335	CD28 inhibiting ph
14	14.8	82.2	18	20 AAX90337	CD28 inhibiting ph
15	13.6	75.6	22	22 AAF16593	Gastric acid produ
16	13.4	74.4	15	24 AAD25952	ASO probe #5 to de
17	13.4	74.4	20	16 AAQ81074	supf gene triplex
18	13.4	74.4	20	16 AAQ81074	Triplex-forming ol
19	13.4	74.4	20	18 AAT70012	Oligonucleotide AG
20	13.4	74.4	20	18 AAT70061	Human JAZF1/JAZ1
21	13.4	74.4	20	24 ABK89176	Human androgen rec
22	13.4	74.4	21	24 AAD30438	Human E1F5 allele-
23	12.8	71.1	16	17 AAT36247	CD28 expression in
24	12.8	71.1	16	20 AAX90340	CD28 inhibiting ph
25	12.8	71.1	17	20 AAV55680	Human tissue Kalli
26	12.8	71.1	17	21 AAF01954	Hammerhead ribozym
27	12.8	71.1	17	24 AAL43484	Human tissue Kalli
28	12.8	71.1	17	24 AAT36245	CD28 expression in
29	12.8	71.1	18	17 AAT36245	Virul integrase in
30	12.8	71.1	18	19 AAX79255	Oligonucleotide #4
31	12.8	71.1	18	20 AAX90338	CD28 inhibiting ph
32	12.8	71.1	19	25 ABX94534	23S/16S rRNA detec
33	12.8	71.1	20	22 AAF72934	Human daxx inhibit
34	12.8	71.1	21	13 AAQ22561	Sry primer (B). H
35	12.8	71.1	21	18 AAV06186	Primer used when o
36	12.8	71.1	21	21 AAA47251	Primer #2 for immu
37	12.8	71.1	22	18 AAT92773	Immunoglobulin lam
38	12.8	71.1	22	19 AAV52770	Ig-lambda #2 PCR p
39	12.8	71.1	22	19 AAV52822	STAR (5' sense) pr
40	12.8	71.1	22	20 AAT22690	Primer 2 for human
41	12.8	71.1	22	21 AAA09933	Primer for human i
42	12.8	71.1	22	21 AAA09933	Primer for human i
43	12.8	71.1	22	21 AAA10013	PCR primer Ig-lambd
44	12.8	71.1	22	22 AAT17128	Human immunoglobul
45	12.8	71.1	22	24 AAT11926	

ALIGNMENTS

RESULT 1

AAT36196

ID AAT36196 standard; DNA; 18 BP.

XX AAT36196;

AC AAT36196;

XX 25-MAR-2003 (updated)

DT 15-APR-1997 (first entry)

XX DE: Triplex forming oligo targetting CD28 5'-UTR (nt 58-75).

XX Reduction; T cell; CD28; gene expression; immune system;
XX disorder; graft versus host disease; septic shock; viral disease;
XX psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;
XX multiple sclerosis; uveitis; rheumatoid arthritis; 5'-UTR;
XX systemic lupus erythematosus; inflammatory bowel disease;
XX triplex forming; oligonucleotide; 5'-untranslated region; ss
XX Synthetic.
OS Synthetic.
XX WO9624380-A1.
PN 15-AUG-1996.
XX PD
XX 05-FEB-1996; 96WO-US01507.
XX PF
XX 09-FEB-1995; 95US-0387041.
XX PR
XX 18-SEP-1995; 95US-0529878.
XX PR
XX 09-FEB-1995; 95US-0387041.
XX PR
XX 18-SEP-1995; 95US-0529878.
XX PR

USN 5,932,530

```

PA (ICMC ) ICM PHARM INC.
XX
FI Tam RC;
XX
XX WPI; 1996-384228/38.
XX
XX Oligonucleotide which reduces CD28 gene expression in T cells -
PT for treating immune system diseases, e.g. graft vs. host disease,
PT septic shock, psoriasis, etc.
XX
XX Claim 9; Page 54; 77pp; English.
PS
XX The present oligonucleotide reduces T cell CD28 gene expression,
CC useful in the treatment of CD28 mediated diseases, particularly
CC immune system disorders, e.g. graft versus host disease, septic
CC shock, viral disease, psoriasis, type I diabetes mellitus,
CC chryoditis, sarcoides, multiple sclerosis, uveitis, rheumatoid
CC arthritis, systemic lupus erythematosus, inflammatory bowel
CC disease, etc.. Reducing CD28 expression may reduce the effects of
CC antigenic stimulation of CD28 positive T cells, with a consequent
CC reduction in cytokine release.
CC (Updated on 25-MAR-2003 to correct PR field.)
XX
XX Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;
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Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 TTGGAGGGGGTGGTGGGG 18
RESULT 2
AAX90328
ID AAX90328 standard; DNA; 18 BP.
AC AAX90328;
XX
XX 24-SEP-1999 (first entry)
XX
XX CD28 inhibiting phosphorothioate oligonucleotide RT03S.
XX
XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
XX immune system mediated disease; gamma-interferon; IL-8;
XX phosphorothioate; ss.
XX Synthetic.
XX US5932556-A.
XX 03-AUG-1999.
XX 18-SEP-1995; 95US-0529878.
XX 18-SEP-1995; 95US-0529878.
XX (TAMR/) TAM R C.
XX Tam RC;
XX WPI; 1999-443609/37.
XX
XX Treatment of immune system-mediated diseases by inhibiting
PT expression of CD28, IL-2, gamma-interferon or IL-8
XX
XX Claim 5; Column 29; 45pp; English.
XX
XX The present invention describes a method for inhibiting the expression
CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
CC comprises subcutaneous administration of an oligonucleotide (OGN).
CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
CC method. The OGNs are used for the treatment of immune system-mediated
CC diseases.
XX
XX Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;
SQ
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Best Local Similarity 100.0%; Pred. No. 3.1e+02;
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Db 1 TTGGAGGGGGTGGTGGGG 18
RESULT 4
AAX299625
ID AAX299625 standard; DNA; 18 BP.
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XX AAX299625;
AC

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XX 12-JUL-2000 (first entry)
DT
XX Nucleotide sequence of G-motif oligonucleotide GRI.
DE
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XX G-motif oligonucleotide; vaccine; Toxoplasmosis; viral infection;
KW antigen presenting cell activation; natural killer cell; septic shock;
KW cytotoxic T-lymphocyte; inflammation; autoimmune disease;
KW rheumatoid arthritis; Crohn's disease; sarcoidosis; multiple sclerosis;
KW Kawasaki syndrome; graft-versus-host disease; transplant rejection;
KW helper T cell response 1-mediated disease; Lyme arthritis;
KW Streptococcal induced arthritis; chronic inflammatory bowel disease;
KW psoriasis vulgaris; experimental allergic encephalomyelitis;
KW insulin-dependent diabetes mellitus; bacterial infection;
KW parasitic infection; Leishmaniasis; spontaneous abortion; tumour; ss.
XX
OS Synthetic.
XX
XX WO200014217-A2.
XX
XX 16-MAR-2000.
XX
XX 03-SEP-1999; 99WO-EP06502.
XX
XX 03-SEP-1998; 98EP-0116652.
XX
XX (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.
XX
XX Wagner H, Lipford GB, Heeg K;
XX
XX WPI; 2000-256970/22.
XX
XX Compositions comprising G-motif oligonucleotides useful for treating
PT e.g. septic shock, rheumatoid arthritis, diabetes and human
PT immunodeficiency virus infections -
XX
XX Example 14; Page 32; 75pp; English.
XX
XX The present sequence represents a G-motif oligonucleotide of the
CC invention. The specification describes compositions comprising G-motif
CC oligonucleotides. The G-motif oligonucleotides inhibit activation of
CC antigen presenting cells by inhibiting the uptake of DNA by a cell, by
CC stimulating natural killer cells, or by co-stimulating cytotoxic
CC T-lymphocytes. The G-motif oligonucleotides may be used for the
CC productions of vaccines for treating septic shock, inflammation,
CC autoimmune diseases (e.g. rheumatoid arthritis, Crohn's disease,
CC sarcoidosis, multiple sclerosis, Kawasaki syndrome, graft-versus-host
CC disease and transplant rejection), helper T cell response 1-mediated
CC diseases (e.g. Streptococcal induced arthritis, Lyme arthritis, chronic
CC inflammatory bowel disease, psoriasis vulgaris, experimental allergic
CC encephalomyelitis, and insulin-dependent diabetes mellitus), bacterial
CC infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis),
CC viral infections (e.g. Cytomegalovirus and human immunodeficiency virus
CC (HIV)-infections), spontaneous abortions and tumours. They may also be
CC used to induce proliferation of bone marrow cells, especially macrophage
CC precursor cells.
XX
XX Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;
SQ
Query Match 100.0%; Score 18; DB 21; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGGAGGGGGTGGTGGGG 18
Ddb 1 TTGGAGGGGGTGGTGGGG 18
RESULT 5
AAZ99650/c
ID AAZ99650 standard; DNA; 18 BP.
XX
XX AAZ99650;
AC

```

```

XX 12-JUL-2000 (first entry)
DT
XX Nucleotide sequence of non-G-motif oligonucleotide GRFicomp.
DE
XX
XX G-motif oligonucleotide; vaccine; Toxoplasmosis; viral infection;
KW antigen presenting cell activation; natural killer cell; septic shock;
KW cytotoxic T-lymphocyte; inflammation; autoimmune disease;
KW rheumatoid arthritis; Crohn's disease; sarcoidosis; multiple sclerosis;
KW Kawasaki syndrome; graft-versus-host disease; transplant rejection;
KW helper T cell response 1-mediated disease; Lyme arthritis;
KW Streptococcal induced arthritis; chronic inflammatory bowel disease;
KW psoriasis vulgaris; experimental allergic encephalomyelitis;
KW insulin-dependent diabetes mellitus; bacterial infection;
KW parasitic infection; Leishmaniasis; spontaneous abortion; tumour; ss.
XX
OS Synthetic.
XX
XX WO200014217-A2.
XX
XX 16-MAR-2000.
XX
XX 03-SEP-1999; 99WO-EP06502.
XX
XX 03-SEP-1998; 98EP-0116652.
XX
XX (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.
XX
XX Wagner H, Lipford GB, Heeg K;
XX
XX WPI; 2000-256970/22.
XX
XX Compositions comprising G-motif oligonucleotides useful for treating
PT e.g. septic shock, rheumatoid arthritis, diabetes and human
PT immunodeficiency virus infections -
XX
XX Example 14; Page 32; 75pp; English.
XX
XX The present sequence represents a non-G-motif oligonucleotide of the
CC invention. The specification describes compositions comprising G-motif
CC oligonucleotides. The G-motif oligonucleotides inhibit activation of
CC antigen presenting cells by inhibiting the uptake of DNA by a cell, by
CC stimulating natural killer cells, or by co-stimulating cytotoxic
CC T-lymphocytes. The G-motif oligonucleotides may be used for the
CC productions of vaccines for treating septic shock, inflammation,
CC autoimmune diseases (e.g. rheumatoid arthritis, Crohn's disease,
CC sarcoidosis, multiple sclerosis, Kawasaki syndrome, graft-versus-host
CC disease and transplant rejection), helper T cell response 1-mediated
CC diseases (e.g. Streptococcal induced arthritis, Lyme arthritis, chronic
CC inflammatory bowel disease, psoriasis vulgaris, experimental allergic
CC encephalomyelitis, and insulin-dependent diabetes mellitus), bacterial
CC infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis),
CC viral infections (e.g. Cytomegalovirus and human immunodeficiency virus
CC (HIV)-infections), spontaneous abortions and tumours. They may also be
CC used to induce proliferation of bone marrow cells, especially macrophage
CC precursor cells.
XX
XX Sequence 18 BP; 4 A; 13 C; 0 G; 1 T; 0 other;
SQ
Query Match 100.0%; Score 18; DB 21; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGGAGGGGGTGGTGGGG 18
Ddb 18 TTGGAGGGGGTGGTGGGG 1
RESULT 6
AAT36197
ID AAT36197 standard; DNA; 21 BP.
XX
XX AAT36197;
AC

```

```

XX 25-MAR-2003 (updated)
DT 15-APR-1997 (first entry)
XX
XX Triplex forming oligo targeting CD28 5'-UTR (nt 58-78).
DE
XX Reduction; T cell; CD28; gene expression; treatment; immune system;
KW disorder; graft versus host disease; septic shock; viral disease;
KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;
KW multiple sclerosis; uveitis; rheumatoid arthritis; 5'-UTR;
KW systemic lupus erythematosus; inflammatory bowel disease;
KW triplex forming; oligonucleotide; 5'-untranslated region; ss
XX
XX Synthetic.
OS
XX WO9624380-A1.
XX
XX 15-AUG-1996.
XX
XX 05-FEB-1996; 96WO-US01507.
XX
XX 09-FEB-1995; 95US-0387041.
PR 18-SEP-1995; 95US-0529878.
PR 09-FEB-1995; 95US-0387041.
PR 18-SEP-1995; 95US-0529878.
XX
XX (ICNC ) ICN PHARM INC.
XX
XX Tam RC;
PI
XX WPI; 1996-384228/38.
XX
XX Oligonucleotide which reduces CD28 gene expression in T cells -
PT for treating immune system diseases, e.g. graft vs. host disease,
PT septic shock, psoriasis, etc.
XX
XX Claim 10; Page 54; 77pp; English.
PS
XX The present oligonucleotide reduces T cell CD28 gene expression,
CC useful in the treatment of CD28 mediated diseases, particularly
CC immune system disorders, e.g. graft versus host disease, septic
CC shock, viral disease, psoriasis, type I diabetes mellitus,
CC thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid
CC arthritis, systemic lupus erythematosus, inflammatory bowel
CC disease, etc.. Reducing CD28 expression may reduce the effects of
CC antigenic stimulation of CD28 positive T cells, with a consequent
CC reduction in cytokine release.
CC (Updated on 25-MAR-2003 to correct PR field.)
XX
XX Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;
SQ
Query Match 100.0%; Score 18; DB 17; Length 21;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGTGGTGGGG 18
DB 4 TTGGAGGGGGTGGTGGGG 21

RESULT 7
AAX90329
ID AAX90329 standard; DNA; 21 BP.
XX
XX AAX90329;
AC
XX 24-SEP-1999 (first entry)
DT
XX CD28 inhibiting phosphorothioate oligonucleotide RT04S.
DE
XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
KW immune system mediated disease; gamma-interferon; IL-8;
KW phosphorothioate; ss.

```

```

XX Synthetic.
OS
XX US5932556-A.
PN
XX 03-AUG-1999.
PD
XX 18-SEP-1995; 95US-0529878.
PF
XX 18-SEP-1995; 95US-0529878.
PR
XX (TAMR/) TAM R C.
PA
XX Tam RC;
PI
XX WPI; 1999-443609/37.
DR
XX Treatment of immune system-mediated diseases by inhibiting
PT expression of CD28, IL-2, gamma-interferon or IL-8
XX
XX Example; Column 21; 45pp; English.
PS
XX The present invention describes a method for inhibiting the expression
CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
CC comprises subcutaneous administration of an oligonucleotide (OGN).
CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
CC method. The OGNs are used for the treatment of immune system-mediated
CC diseases. The present sequence represents a CD28 inhibiting
CC phosphorothioate oligonucleotide used in the exemplification of the
CC present invention.
XX
XX Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;
SQ
Query Match 100.0%; Score 18; DB 20; Length 21;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGTGGTGGGG 18
DB 4 TTGGAGGGGGTGGTGGGG 21

RESULT 8
AAX90291
ID AAX90291 standard; DNA; 21 BP.
XX
XX AAX90291;
AC
XX 24-SEP-1999 (first entry)
DT
XX CD28 inhibition oligonucleotide RT04.
DE
XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
KW immune system mediated disease; gamma-interferon; IL-8; ss.
XX
XX Synthetic.
OS
XX US5932556-A.
PN
XX 03-AUG-1999.
PD
XX 18-SEP-1995; 95US-0529878.
PF
XX 18-SEP-1995; 95US-0529878.
PR
XX (TAMR/) TAM R C.
PA
XX Tam RC;
PI
XX WPI; 1999-443609/37.
DR
XX Treatment of immune system-mediated diseases by inhibiting
PT expression of CD28, IL-2, gamma-interferon or IL-8

```

XX PS Claim 6; Column 29; 45pp; English.

XX CC The present invention describes a method for inhibiting the expression

CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method

CC comprises subcutaneous administration of an oligonucleotide (OGN).

CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the

CC method. The OGNs are used for the treatment of immune system-mediated

CC diseases.

XX SQ Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;

Query Match 100.0%; Score 18; DB 20; Length 21;

Best Local Similarity 100.0%; Pred. No. 3e+02; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 0;

OY 1 TTGAGGGGGTGTGGGG 18

Db 4 TTGAGGGGGTGTGGGG 21

RESULT 9

AAT36243

ID AAT36243 standard; DNA; 18 BP.

XX AC AAT36243;

XX 25-MAR-2003 (updated)

DT 16-APR-1997 (first entry)

XX CD28 expression inhibiting oligonucleotide, RT09s.

DE Reduction; T cell; CD28; gene expression; treatment; immune system;

KW disorder; graft versus host disease; septic shock; viral disease;

KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;

KW multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2;

KW systemic lupus erythematosus; inflammatory bowel disease;

KW IL-2; production; antisense; inhibition; ss

XX Synthetic.

XX WO9624380-A1.

XX 15-AUG-1996.

XX 05-FEB-1996; 96WO-US01507.

XX 09-FEB-1995; 95US-0387041.

PR 18-SEP-1995; 95US-0529878.

PR 03-FEB-1995; 95US-0387041.

PR 18-SEP-1995; 95US-0529878.

XX (ICNC) ICN PHARM INC.

PA Tam RC;

XX WPI; 1996-384228/38.

XX Oligonucleotide which reduces CD28 gene expression in T cells -

PT for treating immune system diseases, e.g. graft vs. host disease,

PT septic shock, psoriasis, etc.

XX Example 2; Page 45; 77pp; English.

XX The present oligonucleotide reduces CD28 dependent interleukin-2

CC (IL-2) production and T cell CD28 gene expression, useful in the

CC treatment of CD28 mediated diseases, particularly immune system

CC disorders, e.g. graft versus host disease, septic shock, viral

CC disease, psoriasis, type I diabetes mellitus, thyroiditis,

CC sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis,

CC systemic lupus erythematosus, inflammatory bowel disease, etc..

CC Reducing CD28 expression may reduce the effects of antigenic

CC stimulation of CD28 positive T cells, with a consequent reduction

CC in cytokine release.

CC (Updated on 25-MAR-2003 to correct PR field.)

XX SQ Sequence 18 BP; 2 A; 0 C; 13 G; 3 T; 0 other;

Query Match 91.1%; Score 16.4; DB 17; Length 18;

Best Local Similarity 94.4%; Pred. No. 1.3e+03;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TTGAGGGGGTGTGGGG 18

Db 1 TTGAGGGGGAGGTGGGG 18

RESULT 10

AAX90336

ID AAX90336 standard; DNA; 18 BP.

XX AC AAX90336;

XX 24-SEP-1999 (first entry)

XX CD28 inhibiting phosphorothioate oligonucleotide RT09S.

DE CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;

KW immune system mediated disease; gamma-interferon; IL-8;

KW phosphorothioate; ss.

XX Synthetic.

XX US932556-A.

XX 03-AUG-1999.

XX 18-SEP-1995; 95US-0529878.

PR 18-SEP-1995; 95US-0529878.

XX (TAMR/) TAM R C.

XX Tam RC;

XX WPI; 1999-443609/37.

XX Treatment of immune system-mediated diseases by inhibiting

PT expression of CD28, IL-2, gamma-interferon or IL-8

XX Example; Column 24; 45pp; English.

XX The present invention describes a method for inhibiting the expression

CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method

CC comprises subcutaneous administration of an oligonucleotide (OGN).

CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the

CC method. The OGNs are used for the treatment of immune system-mediated

CC diseases. The present sequence represents a CD28 inhibiting

CC phosphorothioate oligonucleotide used in the exemplification of the

CC present invention.

XX SQ Sequence 18 BP; 2 A; 0 C; 13 G; 3 T; 0 other;

Query Match 91.1%; Score 16.4; DB 20; Length 18;

Best Local Similarity 94.4%; Pred. No. 1.3e+03;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TTGAGGGGGTGTGGGG 18

Db 1 TTGAGGGGGAGGTGGGG 18

RESULT 11

AAT36242

ID AAT36242 standard; DNA; 18 BP.

XX

AC AAT36242;
 DT 25-MAR-2003 (updated)
 DT 16-APR-1997 (first entry)
 XX
 XX CD28 expression inhibiting oligonucleotide, RT05s.
 XX
 XX Reduction; T cell; CD28; gene expression; treatment; immune system;
 KW disorder; graft versus host disease; septic shock; viral disease;
 KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;
 KW multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2;
 KW systemic lupus erythematosus; inflammatory bowel disease;
 KW IL-2; production; antisense; inhibition; ss
 XX
 XX Synthetic.
 OS
 XX WO9624380-A1.
 PN
 XX 15-AUG-1996.
 PD
 XX 05-FEB-1996; 96WO-US01507.
 PF
 XX 09-FEB-1995; 95US-0387041.
 PR
 XX 18-SEP-1995; 95US-0529878.
 PR
 XX 09-FEB-1995; 95US-0387041.
 PR
 XX 18-SEP-1995; 95US-0529878.
 PR
 XX (ICNC) ICN PHARM INC.
 PA
 XX Tam RC;
 PI
 XX WPI; 1996-384228/38.
 DR
 XX Oligo-nucleotide which reduces CD28 gene expression in T cells -
 PT for treating immune system diseases, e.g. graft vs. host disease,
 PT septic shock, psoriasis, etc.
 XX
 XX Example 2; Page 45; 77pp; English.
 PS
 XX The present oligonucleotide reduces CD28 dependent interleukin-2
 CC (IL-2) production and T cell CD28 gene expression, useful in the
 CC treatment of CD28 mediated diseases, particularly immune system
 CC disorders, e.g. graft versus host disease, septic shock, viral
 CC disease, psoriasis, type I diabetes mellitus, thyroiditis,
 CC sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis,
 CC systemic lupus erythematosus, inflammatory bowel disease, etc..
 CC Reducing CD28 expression may reduce the effects of antigenic
 CC stimulation of CD28 positive T cells, with a consequent reduction
 CC in cytokine release.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 18 BP; 3 A; 0 C; 13 G; 2 T; 0 other;
 Query Match 82.2%; Score 14.8; DB 17; Length 18;
 Best Local Similarity 88.9%; Pred. No. 5.2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 TTGGAGGGGGTGGTGGGG 18
 DB 1 TTGGAGGGGGAGGAGGGG 18
 RESULT 12
 ID AAT36244 standard; DNA; 18 BP.
 AC AAT36244;
 AC
 XX 25-MAR-2003 (updated)
 DT 16-APR-1997 (first entry)
 XX
 XX CD28 expression inhibiting oligonucleotide, RT10s.

KW Reduction; T cell; CD28; gene expression; treatment; immune system;
 KW disorder; graft versus host disease; septic shock; viral disease;
 KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;
 KW multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2;
 KW systemic lupus erythematosus; inflammatory bowel disease;
 KW IL-2; production; antisense; inhibition; ss
 XX
 XX Synthetic.
 OS
 XX WO9624380-A1.
 PN
 XX 15-AUG-1996.
 PD
 XX 05-FEB-1996; 96WO-US01507.
 PF
 XX 09-FEB-1995; 95US-0387041.
 PR
 XX 18-SEP-1995; 95US-0529878.
 PR
 XX 09-FEB-1995; 95US-0387041.
 PR
 XX 18-SEP-1995; 95US-0529878.
 PR
 XX (ICNC) ICN PHARM INC.
 PA
 XX Tam RC;
 PI
 XX WPI; 1996-384228/38.
 DR
 XX Oligo-nucleotide which reduces CD28 gene expression in T cells -
 PT for treating immune system diseases, e.g. graft vs. host disease,
 PT septic shock, psoriasis, etc.
 XX
 XX Example 2; Page 45; 77pp; English.
 PS
 XX The present oligonucleotide reduces CD28 dependent interleukin-2
 CC (IL-2) production and T cell CD28 gene expression, useful in the
 CC treatment of CD28 mediated diseases, particularly immune system
 CC disorders, e.g. graft versus host disease, septic shock, viral
 CC disease, psoriasis, type I diabetes mellitus, thyroiditis,
 CC sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis,
 CC systemic lupus erythematosus, inflammatory bowel disease, etc..
 CC Reducing CD28 expression may reduce the effects of antigenic
 CC stimulation of CD28 positive T cells, with a consequent reduction
 CC in cytokine release.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 18 BP; 1 A; 2 C; 11 G; 4 T; 0 other;
 Query Match 82.2%; Score 14.8; DB 17; Length 18;
 Best Local Similarity 88.9%; Pred. No. 5.2e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 TTGGAGGGGGTGGTGGGG 18
 DB 1 TTGGAGGGGGTGGTGGGG 18
 RESULT 13
 ID AAX90335 standard; DNA; 18 BP.
 XX
 XX AAX90335;
 AC
 XX
 XX 24-SEP-1999 (first entry)
 DT
 XX CD28 inhibiting phosphorothioate oligonucleotide RT05s.
 DE
 XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
 KW immune system mediated disease; gamma-interferon; IL-8;
 KW phosphorothioate; ss.
 XX
 XX Synthetic.
 OS
 XX US5932556-A.
 PN
 XX

```

PD 03-AUG-1999.
XX
XX
XX 18-SEP-1995; 95US-0529878.
XX
XX 18-SEP-1995; 95US-0529878.
XX
XX (TAMR/) TAM R C.
XX
XX
XX Tam RC;
XX
XX WPI; 1999-443609/37.
XX
XX Treatment of immune system-mediated diseases by inhibiting
PT expression of CD28, IL-2, gamma-interferon or IL-8
XX
XX Example; Column 24; 45pp; English.
XX
XX The present invention describes a method for inhibiting the expression
CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
CC comprises subcutaneous administration of an oligonucleotide (OGN).
CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
CC method. The OGNs are used for the treatment of immune system-mediated
CC diseases. The present sequence represents a CD28 inhibiting
CC phosphorothioate oligonucleotide used in the exemplification of the
CC present invention.
XX
XX Sequence 18 BP; 3 A; 0 C; 13 G; 2 T; 0 other;
SQ
Query Match 82.2%; Score 14.8; DB 20; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 TTGGAGGGGGTGGTGGGG 18
DB 1 TTGGAGGGGGGAGGGGG 18
RESULT 14
AAX90337
ID AAX90337 standard; DNA; 18 BP.
XX
XX AAX90337;
XX
XX 24-SEP-1999 (first entry)
XX
XX CD28 inhibiting phosphorothioate oligonucleotide RT10S.
XX
XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
KW immune system mediated disease; gamma-interferon; IL-8;
KW phosphorothioate; ss.
XX
XX Synthetic.
XX
XX US5932556-A.
XX
XX 03-AUG-1999.
XX
XX 18-SEP-1995; 95US-0529878.
XX
XX 18-SEP-1995; 95US-0529878.
XX
XX (TAMR/) TAM R C.
XX
XX Tam RC;
XX
XX WPI; 1999-443609/37.
XX
XX Treatment of immune system-mediated diseases by inhibiting
PT expression of CD28, IL-2, gamma-interferon or IL-8
XX
XX Example; Column 24; 45pp; English.
XX
XX The present invention describes a method for inhibiting the expression
CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
CC comprises subcutaneous administration of an oligonucleotide (OGN).
CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
CC method. The OGNs are used for the treatment of immune system-mediated
CC diseases. The present sequence represents a CD28 inhibiting
CC phosphorothioate oligonucleotide used in the exemplification of the
CC present invention.
XX
XX Sequence 18 BP; 3 A; 0 C; 13 G; 2 T; 0 other;
SQ
Query Match 82.2%; Score 14.8; DB 20; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 TTGGAGGGGGTGGTGGGG 18
DB 1 TTGGAGGGGGGAGGGGG 18
RESULT 15
AAF16593
ID AAF16593 standard; DNA; 22 BP.
XX
XX AAF16593;
XX
XX 13-MAR-2001 (first entry)
XX
XX Gastric acid production inhibiting oligonucleotide SEQ ID NO: 79.
XX
XX Gastric acid disturbance; gastric reflux; gastritis; dyspepsia;
KW stomach ulcer; duodenal ulcer; Helicobacter pylori; antisense;
KW DNA-RNA hybrid; ss.
XX
XX Synthetic.
XX
XX WO200071164-A1.
XX
XX 30-NOV-2000.
XX
XX 24-MAY-2000; 2000WO-AU00498.
XX
XX 24-MAY-1999; 99AU-0000510.
XX
XX (TACH/) TACHAS G.
XX
XX Tachas G;
XX
XX WPI; 2001-025093/03.
XX
XX Treating gastric acid disturbance by administering an oligonucleotide
PT which modulates the activity of a polypeptide involved in gastric acid
PT production or secretion.
XX
XX Example 3; Page 145; 164pp; English.
XX
XX The present invention provides oligonucleotides, and methods for their
CC use, which are useful in modulating the action of proteins involved in
CC gastric acid production. The target protein is preferably the histamine
CC H2 receptor or one of the proteins which form part of the gastric proton
CC pump. The sequences and methods of the invention are useful in the
CC treatment of gastric reflux, gastritis, dyspepsia, stomach ulcers,
CC duodenal ulcers and other gastric acid disturbances, most of which are
CC caused by Helicobacter pylori.
XX
XX Sequence 22 BP; 0 A; 0 C; 16 G; 3 T; 3 other;
SQ
Query Match 75.6%; Score 13.6; DB 22; Length 22;
Best Local Similarity 81.2%; Pred. No. 1.5e+04;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 TGGAGGGGGTGGTGGG 17
DB 2 TGGAGGGGGGAGGGGG 17

```

Tue Oct 28 17:07:53 2003

us-09-331-204a-4.szlm22.rng

Page 8

Search completed: October 27, 2003, 11:25:18
Job time : 163 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:29 ; Search time 376.114 Seconds
(without alignments)
1957.844 Million cell updates/sec

Title: US-09-331-204A-5
Perfect score: 18
Sequence: 1 9999agaggggctggaa 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues
Total number of hits satisfying chosen parameters: 581044

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:**

1: gb_ba:**
2: gb_htg:**
3: gb_in:**
4: gb_em:**
5: gb_ov:**
6: gb_pat:**
7: gb_ph:**
8: gb_pl:**
9: gb_pr:**
10: gb_ro:**
11: gb_sts:**
12: gb_sy:**
13: gb_un:**
14: gb_vi:**
15: em_ba:**
16: em_fun:**
17: em_hum:**
18: em_in:**
19: em_mu:**
20: em_om:**
21: em_or:**
22: em_ov:**
23: em_pat:**
24: em_ph:**
25: em_pl:**
26: em_ro:**
27: em_sts:**
28: em_un:**
29: em_vi:**
30: em_htg_hum:**
31: em_htg_inv:**
32: em_htg_other:**
33: em_htg_mus:**
34: em_htg_pln:**
35: em_htg_rod:**
36: em_htg_mam:**
37: em_htg_vrt:**
38: em_sy:**
39: em_htgo_hum:**
40: em_htgo_mus:**
41: em_htgo_other:**

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
C 1	13.8	76.7	17	6	AR029939	Sequence
C 2	13.8	76.7	21	6	AX096246	Sequence
C 3	13.4	74.4	20	6	AR103774	Sequence
C 4	13.4	74.4	20	6	BD130004	Ashma-as
C 5	13.4	74.4	22	6	A27787	Oligonucleo
C 6	12.8	71.1	17	6	AX215456	Sequence
C 7	12.8	71.1	17	6	AX215457	Sequence
C 8	12.8	71.1	17	6	AX422501	Sequence
C 9	12.8	71.1	17	6	AX422502	Sequence
C 10	12.8	71.1	19	6	AX001112	Sequence
C 11	12.8	71.1	20	6	AR029133	Sequence
C 12	12.8	71.1	20	6	AR036517	Sequence
C 13	12.8	71.1	20	6	AR073952	Sequence
C 14	12.8	71.1	20	6	AR096050	Sequence
C 15	12.8	71.1	20	6	AR105507	Sequence
C 16	12.8	71.1	20	6	AR212283	Sequence
C 17	12.8	71.1	20	6	AR215974	Sequence
C 18	12.8	71.1	20	6	AR231417	Sequence
C 19	12.8	71.1	20	6	E49531	Antisense o
C 20	12.8	71.1	20	6	I27251	Sequence 21
C 21	12.8	71.1	22	6	A4397	Sequence 27
C 22	12.8	71.1	22	6	AR193523	Sequence
C 23	12.4	68.9	17	6	AX532422	Sequence
C 24	12.4	68.9	17	6	AX532423	Sequence
C 25	12.4	68.9	17	6	AX532424	Sequence
C 26	12.4	68.9	17	6	AX532425	Sequence
C 27	12.4	68.9	18	6	A97983	Sequence 13
C 28	12.4	68.9	20	6	AR208749	Sequence
C 29	12.4	68.9	20	6	AR208750	Sequence
C 30	12.4	68.9	21	6	BD173872	Novel pro
C 31	12.2	67.8	17	6	AX216967	Sequence
C 32	12.2	67.8	18	6	A97312	Sequence 29
C 33	12.2	67.8	19	6	AX119341	Sequence
C 34	12.2	67.8	20	6	AR080189	Sequence
C 35	12.2	67.8	20	6	AX664949	Sequence
C 36	12.2	67.8	20	6	I60656	Sequence 6
C 37	12.2	66.7	16	6	I26792	Sequence 15
C 38	12.2	66.7	16	6	I91533	Sequence 15
C 39	12.2	66.7	17	6	AR029938	Sequence
C 40	12.2	66.7	17	6	AX214604	Sequence
C 41	12.2	66.7	17	6	AX214605	Sequence
C 42	12.2	66.7	17	6	AX215458	Sequence
C 43	12.2	66.7	17	6	AX215459	Sequence
C 44	12.2	66.7	17	6	AX532426	Sequence
C 45	12.2	66.7	17	6	AX532427	Sequence

ALIGNMENTS

RESULT 1
AR029939/C
LOCUS AR029939 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 128 from patent US 5861244.
ACCESSION AR029939
VERSION AR029939.1 GI:5943153
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Wang, C.-G. and Hepburn, A.G.
TITLE Genetic sequence assay using DNA triple strand formation
JOURNAL Patent: US 5861244-A 128 19-JAN-1999;
FEATURES Location/Qualifiers

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/organism="unknown"
BASE COUNT 0 a 12 c 0 g 5 t
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Best Local Similarity 88.2%; Pred. No. 1.8e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGGA 17
Db 17 GGGGAGGAGGGGAAGGA 1

RESULT 2
AX096246/c
LOCUS
DEFINITION Sequence 1424 from Patent WO0118250.
ACCESSION AX096246
VERSION AX096246.1 GI:13512473
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Lander, E.S., Gargill, M., Ireland, J.S., Bolck, S., Daley, G.Q. and
McCarthy, J.J.
TITLE Single nucleotide polymorphisms in genes
JOURNAL Patent: WO 0118250-A 1424 15-MAR-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US); Millennium
Pharmaceuticals, Inc. (US)

FEATURES
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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BASE COUNT 2 a 1 g 5 t 1 others
ORIGIN

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Best Local Similarity 88.2%; Pred. No. 1.7e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGGA 17
Db 21 GGGGAGGAGGCTGGA 5

RESULT 3
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LOCUS
DEFINITION Sequence 298 from patent US 6087485.
ACCESSION AR103774
VERSION AR103774.1 GI:12815362
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Brooks-Wilson, A.R., Buckler, A., Cardon, L., Carey, A.H., Galvin, M.,
Miller, A. and North, M.

TITLE Asthma related genes
JOURNAL Patent: US 6087485-A 298 11-JUL-2000;
FEATURES
source
1..20
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BASE COUNT 3 a 2 c 12 g 3 t
ORIGIN

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Best Local Similarity 93.3%; Pred. No. 2.6e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTG 15
Db 5 GGTGAGGAGGGGCTG 19

RESULT 4
BD130004
LOCUS
DEFINITION Asthma-associated gene.
ACCESSION BD130004
VERSION BD130004.1 GI:23224949
KEYWORDS JP 2002500895-A/294.
SOURCE unidentified
ORGANISM unidentified
unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Wilson, A.R.B., Buckler, A., Cardon, L., Carey, A.H., Galvin, M.,
Miller, A. and North, M.
TITLE Asthma-associated gene
JOURNAL Patent: JP 2002500895-A 294 15-JAN-2002;
COMMENT OS Unidentified
PN JP 2002500895-A/294
PD 15-JAN-2002
PF 21-JAN-1998 JP 2000528715
PI ANGELA R. BROOKS WILSON, ALAN BUCKLER, LON
CARDON, ALI SUD H CAREY,
PI MARGARET GALVIN, ANDREW MILLER, MICHAEL NORTH
PC C1Q1/68.A01K67/027, C07K14/47, C12N15/09, C12N15/00 CC
Strandedness: Single;
CC Topology: Linear;
CC Asthma-associated gene
FH Key Location/Qualifiers
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FI /organism="Unidentified".

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/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT 3 a 2 c 12 g 3 t
ORIGIN

Query Match 74.4%; Score 13.4; DB 6; Length 20;
Best Local Similarity 93.3%; Pred. No. 2.6e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTG 15
Db 5 GGTGAGGAGGGGCTG 19

RESULT 5
A27787
LOCUS
DEFINITION Oligonucleotide DNA (33.6 AL) from patent EP0422861.
ACCESSION A27787
VERSION A27787.1 GI:905260
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1 (bases 1 to 22)
AUTHORS Garman, A.J.
TITLE Probes
JOURNAL Patent: EP 0422861-A 1 17-APR-1991;
IMPERIAL CHEMICAL INDUSTRIES PLC; ZENECA LIMITED
FEATURES
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Best Local Similarity 93.3%; Pred. No. 2.6e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db   2 GGAGGAAGGCTGGA 16

RESULT 6
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LOCUS      AX215456
DEFINITION Sequence 898 from Patent WO0159103.
ACCESSION  AX215456
VERSION     AX215456.1 GI:15525499
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1
AUTHORS    Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE      Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL    nogo gene expression
PUBLISHED  Patent: WO 0159103-A 898 16-AUG-2001;
RIBOZYME   PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES   source
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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db   17 GGGAGGAGGGGCTGG 2

RESULT 7
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LOCUS      AX215457
DEFINITION Sequence 899 from Patent WO0159103.
ACCESSION  AX215457
VERSION     AX215457.1 GI:15525500
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1
AUTHORS    Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE      Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL    nogo gene expression
PUBLISHED  Patent: WO 0159103-A 899 16-AUG-2001;
RIBOZYME   PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES   source
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            Location/Qualifiers
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BASE COUNT      0 a      14 c      0 g      3 t
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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Best Local Similarity 87.5%; Pred. No. 4.9e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  1 GGGAGGAGGGGCTGG 16
    ||||| ||||| ||
Db   16 GGGAGGAGGGGCTGG 1

RESULT 8
AX422501/c
LOCUS      AX422501
DEFINITION Sequence 837 from Patent WO0188124.
ACCESSION  AX422501
VERSION     AX422501.1 GI:21525883
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Jarvis, T., von Carlowitz, I., McSwiggen, J.A., McLaughlin, F.G. and
TITLE      Method and reagent for the inhibition of erg
JOURNAL    Patent: WO 0188124-A 837 22-NOV-2001;
RIBOZYME   PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES   source
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                /mol_type="mRNA"
                /db_xref="taxon:9606"
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Best Local Similarity 87.5%; Pred. No. 4.9e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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    ||||| ||||| ||
Db   17 GGGAGGAGGGGCTGGA 2

RESULT 9
AX422502/c
LOCUS      AX422502
DEFINITION Sequence 838 from Patent WO0188124.
ACCESSION  AX422502
VERSION     AX422502.1 GI:21525884
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Jarvis, T., von Carlowitz, I., McSwiggen, J.A., McLaughlin, F.G. and
TITLE      Method and reagent for the inhibition of erg
JOURNAL    Patent: WO 0188124-A 838 22-NOV-2001;
RIBOZYME   PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES   source
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                /db_xref="taxon:9606"
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ORIGIN

Query Match      71.1%; Score 12.8; DB 6; Length 17;
Best Local Similarity 87.5%; Pred. No. 4.9e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db   2 GGGAGGAGGGGCTGGA 17

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10

Qy 1 GGGGAGGAGGGCTGG 16
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Db 20 GGGGAGGAGGCGGG 5

RESULT 15
AR105507/c
LOCUS AR105507 20 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 7 from patent US 6096720.
ACCESSION AR105507
VERSION AR105507.1 GI:12819104
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Love,W.Guy., Nicklin,P.Leslie., Hamilton,K.Ophelia. and Phillips,J.Ann.
TITLE Liposomal oligonucleotide compositions
JOURNAL Patent: US 6096720-A 7 01-AUG-2000;
FEATURES
source 1..20
/organism="unknown"
BASE COUNT 0 a 14 c 2 g 4 t
ORIGIN

Query Match 71.1%; Score 12.8; DB 6; Length 20;
Best Local Similarity 87.5%; Pred.No. 4.7e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGGAGGAGGGCTGG 16
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Db 20 GGGGAGGAGGCGGG 5

Search completed: October 27, 2003, 11:09:24
Job time : 378.114 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:29 ; Search time 162 Seconds
(without alignments)
299.938 Million cell updates/sec

Title: US-09-331-204A-5
Perfect score: 18
Sequence: 1 gggaggaggggctgaa 18
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 1643890

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_19Jun03.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	18	100.0	18	17	AAT36241
2	18	100.0	18	17	AAT36255
3	18	100.0	18	20	AA190334
4	18	100.0	18	20	AA190346
5	13.8	76.7	17	20	AA14741
6	13.8	76.7	18	15	AAQ70343
7	13.8	76.7	21	15	AAQ70342
8	13.8	76.7	21	15	AAQ70345

C	9	13.8	76.7	21	22	AAF96659	Human gene single
10	13.4	74.4	74.4	20	20	AAZ18648	ASTH1 gene intron/
11	13.4	74.4	74.4	20	21	AAA93151	Clone vgl5.1 seque
12	13.4	74.4	74.4	20	21	AA80555	Human ASTH1 gene
13	13	72.2	72.2	21	21	AA68417	Primer #2 used to
14	12.8	71.1	71.1	17	23	ABK00898	Human NOGO inozyme
15	12.8	71.1	71.1	17	23	ABK00899	Human NOGO inozyme
16	12.8	71.1	71.1	17	24	ABN07492	Human GDMPLP-1 17-m
17	12.8	71.1	71.1	17	24	ABN07493	Human GDMPLP-1 17-m
18	12.8	71.1	71.1	17	24	ABK18190	Human ERG hammarhe
19	12.8	71.1	71.1	17	24	ABK18191	Human ERG hammarhe
20	12.8	71.1	71.1	20	17	AAK17501	Human c-raf kinase
21	12.8	71.1	71.1	20	18	AAK36460	Chimeric 2'-O-meth
22	12.8	71.1	71.1	20	18	AAK36460	Human c-raf and de
23	12.8	71.1	71.1	20	18	AAK36460	Human c-raf kinase
24	12.8	71.1	71.1	20	20	AAZ10292	Oligonucleotide us
25	12.8	71.1	71.1	20	20	AAZ10292	Chimeric antisense
26	12.8	71.1	71.1	20	20	AAK05464	c-raf antisense ch
27	12.8	71.1	71.1	20	20	AAK15066	Human c-raf kinase
28	12.8	71.1	71.1	20	21	AAK73509	Human c-raf kinase
29	12.8	71.1	71.1	20	21	AAZ48162	C-raf chimeric Pho
30	12.8	71.1	71.1	20	24	AAZ48162	Human c-raf kinase
31	12.8	71.1	71.1	22	16	AAQ86739	Human FGF receptor
32	12.8	71.1	71.1	22	19	AAK99482	Human ST receptor
33	12.8	71.1	71.1	22	19	AAK99486	Human ST receptor
34	12.8	71.1	71.1	22	19	AAK99486	Human ST receptor
35	12.8	71.1	71.1	22	19	AAK99486	Human ST receptor
36	12.8	71.1	71.1	22	19	AAK99486	Human ST receptor
37	12.8	71.1	71.1	22	24	AAK46753	FGF receptor antis
38	12.4	68.9	68.9	15	22	AAH91757	Human inflammatory
39	12.4	68.9	68.9	17	24	ABV91218	Human POSHL1 scann
40	12.4	68.9	68.9	17	24	ABV91219	Human POSHL1 scann
41	12.4	68.9	68.9	17	24	ABV91220	Human POSHL1 scann
42	12.4	68.9	68.9	17	24	ABV91221	Human POSHL1 scann
43	12.4	68.9	68.9	17	24	ABN07494	Human GDMPLP-1 17-m
44	12.4	68.9	68.9	17	24	ABN07495	Human GDMPLP-1 17-m
45	12.4	68.9	68.9	18	20	AAK23093	Primer #16. Synth

ALIGNMENTS

RESULT 1
AAT36241
ID AAT36241 standard; DNA; 18 BP.
XX
XX AAT36241;
XX AC
XX 25-MAR-2003 (updated)
DT 16-APR-1997 (first entry)
XX
XX CD28 expression inhibiting oligonucleotide, RTILs.
DE
XX Reduction; T cell; CD28; gene expression; treatment; immune system;
KW disorder; graft versus host disease; septic shock; viral disease;
KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;
KW multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2;
KW systemic lupus erythematosus; inflammatory bowel disease;
KW IL-2; production; antisense; inhibition; ss
XX
XX Synthetic.
XX
XX WO9624380-A1.
XX
XX 15-AUG-1996.
XX
XX 05-FEB-1996; 96WO-US01507.
XX
XX 09-FEB-1995; 95US-0387041.
PR 18-SEP-1995; 95US-0529878.
PR 09-FEB-1995; 95US-0387041.
PR 18-SEP-1995; 95US-0529878.
XX

PA (ICNC) ICN PHARM INC.
 XX Tam RC;
 PI
 DR WPI; 1996-384228/38.
 XX
 PT Oligo:nucleotide which reduces CD28 gene expression in T cells -
 XX for treating immune system diseases, e.g. graft vs. host disease,
 PT septic shock, psoriasis, etc.
 XX
 PS Example 2; Page 45; 77pp; English.
 XX
 CC The present oligonucleotide reduces CD28 dependent interleukin-2
 CC (IL-2) production and T cell CD28 gene expression, useful in the
 CC treatment of CD28 mediated diseases, particularly immune system
 CC disorders, e.g. graft versus host disease, septic shock, viral
 CC disease, psoriasis, type I diabetes mellitus, thyroiditis,
 CC sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis,
 CC systemic lupus erythematosus, inflammatory bowel disease, etc..
 CC Reducing CD28 expression may reduce the effects of antigenic
 CC stimulation of CD28 positive T cells, with a consequent reduction
 CC in cytokine release.
 CC (Updated on 25-MAR-2003 to correct PR field.)
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 SQ Sequence 18 BP; 4 A; 1 C; 12 G; 1 T; 0 other;
 Query Match 100.0%; Score 18; DB 17; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGGAA 18
 DB 1 GGGGAGGAGGGGCTGGAA 18

RESULT 2
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 ID AAT36255 standard; DNA; 18 BP.
 XX
 AC AAT36255;
 XX
 DT 25-MAR-2003 (updated)
 DT 16-APR-1997 (first entry)
 XX
 DE CD28 expression inhibiting oligonucleotide, RT06s.
 XX
 KW Reduction; T cell; CD28; gene expression; treatment; immune system;
 KW disorder; graft versus host disease; septic shock; viral disease;
 KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;
 KW multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2;
 KW systemic lupus erythematosus; inflammatory bowel disease;
 KW IL-2; production; antisense; inhibition; ss
 OS Synthetic.
 XX
 XX WC9624380-A1.
 PN
 XX
 PD 15-AUG-1996.
 XX
 XX 05-FEB-1996; 96WO-US01507.
 PF
 XX 09-FEB-1995; 95US-0387041.
 PR 18-SEP-1995; 95US-0529878.
 PR 09-FEB-1995; 95US-0387041.
 PR 18-SEP-1995; 95US-0529878.
 XX
 XX (ICNC) ICN PHARM INC.
 PA
 XX Tam RC;
 PI
 XX WPI; 1996-384228/38.
 DR
 XX Oligo:nucleotide which reduces CD28 gene expression in T cells -

PT for treating immune system diseases, e.g. graft vs. host disease,
 XX septic shock, psoriasis, etc.
 PS Example 2; Page 45; 77pp; English.
 XX
 CC The present oligonucleotide reduces CD28 dependent interleukin-2
 CC (IL-2) production and T cell CD28 gene expression, useful in the
 CC treatment of CD28 mediated diseases, particularly immune system
 CC disorders, e.g. graft versus host disease, septic shock, viral
 CC disease, psoriasis, type I diabetes mellitus, thyroiditis,
 CC sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis,
 CC systemic lupus erythematosus, inflammatory bowel disease, etc..
 CC Reducing CD28 expression may reduce the effects of antigenic
 CC stimulation of CD28 positive T cells, with a consequent reduction
 CC in cytokine release.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 18 BP; 1 A; 12 C; 1 G; 4 T; 0 other;
 Query Match 100.0%; Score 18; DB 17; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGGAA 18
 DB 18 GGGGAGGAGGGGCTGGAA 1

RESULT 3
 AAX90334
 ID AAX90334 standard; DNA; 18 BP.
 XX
 AC AAX90334;
 XX
 DT 24-SEP-1999 (first entry)
 DT
 XX
 DE CD28 inhibiting phosphorothioate oligonucleotide RT11s.
 XX
 KW CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
 KW immune system mediated disease; gamma-interferon; IL-8;
 KW phosphorothioate; ss.
 XX
 OS Synthetic.
 XX
 PN US5932556-A.
 XX
 PD 03-AUG-1999.
 XX
 PF 18-SEP-1995; 95US-0529878.
 XX
 PR 18-SEP-1995; 95US-0529878.
 XX
 XX (TAMR/) TAM R C.
 PA
 XX Tam RC;
 PI
 XX WPI; 1999-443609/37.
 DR
 XX Treatment of immune system-mediated diseases by inhibiting
 PT expression of CD28, IL-2, gamma-interferon or IL-8
 XX
 PS Example; Column 24; 45pp; English.
 XX
 CC The present invention describes a method for inhibiting the expression
 CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
 CC comprises subcutaneous administration of an oligonucleotide (OGN).
 CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
 CC method. The OGNs are used for the treatment of immune system-mediated
 CC diseases. The present sequence represents a CD28 inhibiting
 CC phosphorothioate oligonucleotide used in the exemplification of the
 CC present invention.
 XX
 SQ Sequence 18 BP; 4 A; 1 C; 12 G; 1 T; 0 other;

Query Match 100.0%; Score 18; DB 20; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGGAA 18
 |||||
 Db 1 GGGGAGGAGGGGCTGGAA 18

RESULT 4

AAAX90346/c
 ID AAAX90346 standard; DNA; 18 BP.

AC AAAX90346;

DT 24-SEP-1999 (first entry)

XX CD28 inhibiting phosphorothioate oligonucleotide RT06S.

XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
 KW immune system mediated disease; gamma-interferon; IL-8;
 KW phosphorothioate; ss.

OS Synthetic.

XX US5932556-A.

PN 03-AUG-1999.

PD 18-SEP-1995; 95US-0529878.

XX 18-SEP-1995; 95US-0529878.

XX (TAMR/) TAM R C.

PA Tam RC;

PI WPI; 1999-443609/37.

XX Treatment of immune system-mediated diseases by inhibiting
 PT expression of CD28, IL-2, gamma-interferon or IL-8

XX Example; Column 24; 45pp; English.

XX The present invention describes a method for inhibiting the expression
 CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
 CC comprises subcutaneous administration of an oligonucleotide (OGN).
 CC AAAX90288 to AAAX90291 represent specifically claimed OGNs for use in the
 CC method. The OGNs are used for the treatment of immune system-mediated
 CC diseases. The present sequence represents a CD28 inhibiting
 CC phosphorothioate oligonucleotide used in the exemplification of the
 CC present invention.

XX Sequence 18 BP; 1 A; 12 C; 1 G; 4 T; 0 other;

Query Match 100.0%; Score 18; DB 20; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGGAA 18
 |||||
 Db 18 GGGGAGGAGGGGCTGGAA 1

RESULT 5

AAAX14741/c

ID AAAX14741 standard; DNA; 17 BP.

XX AAAX14741;

XX 24-MAR-1999 (first entry)

XX

DE Triple helix third strand of alpha-globin gene nucleotides 827-843.
 XX Triple helix formation; DNA detection; triple helix; identification;
 KW bacteria; oncogene; virus; ss.
 XX Synthetic.
 OS Homo sapiens.
 XX US5861244-A.
 XX 19-JAN-1999.
 PD 22-DEC-1993; 93US-0173489.
 XX 22-DEC-1993; 93US-0173489.
 PR 29-OCT-1992; 92US-0968436.
 XX (PROF-) PROFILE DIAGNOSTIC SCI INC.
 PA Hepburn AG, Wang C;
 XX WPI; 1999-130384/11.
 DR Assay of genetic sequences based on triplex formation from double
 PT stranded analyte - and hybrid of anchor and reporter sequences, with
 PT reporter released if triplex formation occurs, used e.g. to identify
 PT bacteria
 XX Disclosure; Columns 17-18; 168pp; English.
 XX The present sequence represents a polynucleotide that is able to
 CC form a triple helix with a double stranded sequence. Cytosine bases
 CC in the present can be replaced with 5-methylcytosine for increased
 CC triplex stability. The present sequence is used in the assay of the
 CC invention, where it can be part of the anchor DNA or reporter DNA
 CC sequence. The assay comprises adding a sample containing double-stranded
 CC DNA test sequences to an aqueous medium containing at least one complex
 CC of anchor DNA, attached to a solid support, and reporter DNA, where
 CC either a part of the anchor DNA or reporter DNA is designed to form
 CC a triple-strand structure with part of the test sequence. Triplex
 CC formation results in displacement of the reporter DNA which is
 CC detected as an indication of the presence of the DNA test sequence.
 CC The method is used to detect DNA sequences, particularly for
 CC identification of bacteria (by detecting genes for ribosomal RNA) in
 CC clinical samples, but also detection of oncogenes and Hepatitis B virus.
 XX Sequence 17 BP; 0 A; 12 C; 0 G; 5 T; 0 other;
 SQ Query Match 76.7%; Score 13.8; DB 20; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.5e+04;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGGA 17
 |||||
 Db 17 GGGGAGGAGGGGGAAGA 1

RESULT 6
 AAQ70343/c
 ID AAQ70343 standard; DNA; 18 BP.
 XX
 AC AAQ70343;
 XX
 DT 25-MAR-2003 (updated)
 DT 15-FEB-1995 (first entry)
 XX
 DE Antisense oligonucleotide for mouse FGF.
 XX Fibroblast growth factor; hybridisation; laser procedures;
 KW vascular smooth muscle cell; proliferation;
 KW SMC; vascular stenosis; post angioplasty restenosis;
 KW atherosclerosis; cardiac hypertrophy; organ transplant; ss.
 XX

DR MPI; 1994-249123/30.

XX New anti-sense polynucleotide(s) to fibroblast growth factor

PT receptor - used for inhibiting vascular smooth muscle cell

PT proliferation, partic. for treating restenosis

XX

PS Claim 3; Page 9; 53pp; English.

XX

CC The sequence is an antisense molecule directed against position -3

CC to +18, relative to the start codon of the gene for

CC mouse fibroblast growth factor 1. The polynucleotide can be used for

CC inhibiting vascular smooth muscle cell proliferation and for treating

CC a disease e.g. vascular stenosis, post angioplasty restenosis,

CC atherectomy, atherosclerosis, atrial venous shunt failure, cardiac

CC hyper trophy, vascular surgery and organ transplant.

CC See also AAQ70333-60.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX

XX Sequence 21 BP; 4 A; 12 C; 2 G; 3 T; 0 other;

XX

Query Match 76.7%; Score 13.8; DB 15; Length 21;

Best Local Similarity 88.2%; Pred. No. 1.5e+04;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps

QY 2 GGGAGGAGGGCTGGAA 18

DB 21 GGGATGTGGGCTGGAA 5

RESULT 8

AAQ70345/c

ID AAQ70345 standard; DNA; 21 BP.

XX

AC AAQ70345;

XX

DT 25-MAR-2003 (updated)

DT 15-FEB-1995 (first entry)

XX

DE Antisense oligonucleotide for mouse POF.

XX

KW Fibroblast growth factor; hybridisation; laser procedures;

KW vascular smooth muscle cell; proliferation;

KW SMC; vascular stenosis; post angioplasty restenosis;

KW atherosclerosis; cardiac hypertrophy; organ transplant; ss.

XX

OS Synthetic.

XX

PN W09415945-A1.

XX

PD 21-JUL-1994.

XX

PF 28-DEC-1993; 93WO-US12600.

XX

PR 31-DEC-1992; 92US-0999706.

XX

PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.

XX

PI Denner LA, Dixon RAF, Rege AA, Dixon RA;

XX

DR MPI; 1994-249123/30.

XX

CC New anti-sense polynucleotide(s) to fibroblast growth factor

PT receptor - used for inhibiting vascular smooth muscle cell

PT proliferation, partic. for treating restenosis

XX

PS Claim 3; Page 9; 53pp; English.

XX

CC The sequence is an antisense molecule directed against position -6

CC to +15, relative to the start codon of the gene for

CC mouse fibroblast growth factor 1. The polynucleotide can be used for

CC inhibiting vascular smooth muscle cell proliferation and for treating

CC a disease e.g. vascular stenosis, post angioplasty restenosis,

CC atherectomy, atherosclerosis, atrial venous shunt failure, cardiac

CC hyper trophy, vascular surgery and organ transplant.

CC See also AAQ70333-60.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX

XX Sequence 21 BP; 4 A; 12 C; 2 G; 3 T; 0 other;

XX

Query Match 76.7%; Score 13.8; DB 15; Length 21;

Best Local Similarity 88.2%; Pred. No. 1.5e+04;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps

QY 2 GGGAGGAGGGCTGGAA 18

DB 21 GGGATGTGGGCTGGAA 5

RESULT 8

AAQ70345/c

ID AAQ70345 standard; DNA; 21 BP.

XX

AC AAQ70345;

XX

DT 25-MAR-2003 (updated)

DT 15-FEB-1995 (first entry)

XX

DE Antisense oligonucleotide for mouse POF.

XX

KW Fibroblast growth factor; hybridisation; laser procedures;

KW vascular smooth muscle cell; proliferation;

KW SMC; vascular stenosis; post angioplasty restenosis;

KW atherosclerosis; cardiac hypertrophy; organ transplant; ss.

XX

OS Synthetic.

XX

PN W09415945-A1.

XX

PD 21-JUL-1994.

XX

PF 28-DEC-1993; 93WO-US12600.

XX

PR 31-DEC-1992; 92US-0999706.

XX

PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.

XX

PI Denner LA, Dixon RAF, Rege AA, Dixon RA;

XX

DR MPI; 1994-249123/30.

XX

CC New anti-sense polynucleotide(s) to fibroblast growth factor

PT receptor - used for inhibiting vascular smooth muscle cell

PT proliferation, partic. for treating restenosis

XX

PS Claim 3; Page 9; 53pp; English.

XX

CC The sequence is an antisense molecule directed against position -6

CC to +15, relative to the start codon of the gene for

CC mouse fibroblast growth factor 1. The polynucleotide can be used for

CC inhibiting vascular smooth muscle cell proliferation and for treating

CC a disease e.g. vascular stenosis, post angioplasty restenosis,

CC atherectomy, atherosclerosis, atrial venous shunt failure, cardiac

CC hyper trophy, vascular surgery and organ transplant.

CC See also AAQ70333-60.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX

XX Sequence 21 BP; 4 A; 12 C; 2 G; 3 T; 0 other;

XX

Query Match 76.7%; Score 13.8; DB 15; Length 21;

Best Local Similarity 88.2%; Pred. No. 1.5e+04;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps

QY 2 GGGAGGAGGGCTGGAA 18

DB 21 GGGATGTGGGCTGGAA 5

RESULT 8

AAQ70345/c

ID AAQ70345 standard; DNA; 21 BP.

XX

AC AAQ70345;

XX

DT 25-MAR-2003 (updated)

DT 15-FEB-1995 (first entry)

XX

DE Antisense oligonucleotide for mouse POF.

XX

KW Fibroblast growth factor; hybridisation; laser procedures;

KW vascular smooth muscle cell; proliferation;

KW SMC; vascular stenosis; post angioplasty restenosis;

KW atherosclerosis; cardiac hypertrophy; organ transplant; ss.

XX

OS Synthetic.

XX

PN W09415945-A1.

XX

PD 21-JUL-1994.

XX

PF 28-DEC-1993; 93WO-US12600.

XX

PR 31-DEC-1992; 92US-0999706.

XX

PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.

XX

PI Denner LA, Dixon RAF, Rege AA, Dixon RA;

XX

DR MPI; 1994-249123/30.

XX

CC New anti-sense polynucleotide(s) to fibroblast growth factor

PT receptor - used for inhibiting vascular smooth muscle cell

PT proliferation, partic. for treating restenosis

XX

PS Claim 3; Page 9; 53pp; English.

XX

CC The sequence is an antisense molecule directed against position -6

CC to +15, relative to the start codon of the gene for

CC mouse fibroblast growth factor 1. The polynucleotide can be used for

CC inhibiting vascular smooth muscle cell proliferation and for treating

CC a disease e.g. vascular stenosis, post angioplasty restenosis,

CC atherectomy, atherosclerosis, atrial venous shunt failure, cardiac

CC hyper trophy, vascular surgery and organ transplant.

CC See also AAQ70333-60.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX

XX Sequence 21 BP; 4 A; 12 C; 2 G; 3 T; 0 other;

XX

Query Match 76.7%; Score 13.8; DB 15; Length 21;

Best Local Similarity 88.2%; Pred. No. 1.5e+04;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps

QY 2 GGGAGGAGGGCTGGAA 18

DB 21 GGGATGTGGGCTGGAA 5

RESULT 8

AAQ70345/c

ID AAQ70345 standard; DNA; 21 BP.

XX

AC AAQ70345;

XX

DT 25-MAR-2003 (updated)

DT 15-FEB-1995 (first entry)

XX

DE Antisense oligonucleotide for mouse POF.

XX

KW Fibroblast growth factor; hybridisation; laser procedures;

KW vascular smooth muscle cell; proliferation;

KW SMC; vascular stenosis; post angioplasty restenosis;

KW atherosclerosis; cardiac hypertrophy; organ transplant; ss.

XX

OS Synthetic.

XX

PN W09415945-A1.

XX

PD 21-JUL-1994.

XX

PF 28-DEC-1993; 93WO-US12600.

XX

PR 31-DEC-1992; 92US-0999706.

XX

PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.

XX

PI Denner LA, Dixon RAF, Rege AA, Dixon RA;

XX

DR MPI; 1994-249123/30.

XX

CC New anti-sense polynucleotide(s) to fibroblast growth factor

PT receptor - used for inhibiting vascular smooth muscle cell

PT proliferation, partic. for treating restenosis

XX

PS Claim 3; Page 9; 53pp; English.

XX

CC The sequence is an antisense molecule directed against position -6

CC to +15, relative to the start codon of the gene for

CC mouse fibroblast growth factor 1. The polynucleotide can be used for

CC inhibiting vascular smooth muscle cell proliferation and for treating

CC a disease e.g. vascular stenosis, post angioplasty restenosis,

CC atherectomy, atherosclerosis, atrial venous shunt failure, cardiac

CC hyper trophy, vascular surgery and organ transplant.

CC See also AAQ70333-60.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX

XX Sequence 21 BP; 4 A; 12 C; 2 G; 3 T; 0 other;

XX

Query Match 76.7%; Score 13.8; DB 15; Length 21;

Best Local Similarity 88.2%; Pred. No. 1.5e+04;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps

QY 2 GGGAGGAGGGCTGGAA 18

DB 21 GGGATGTGGGCTGGAA 5

RESULT 8

AAQ70345/c

ID AAQ70345 standard; DNA; 21 BP.

XX

AC AAQ70345;

XX

DT 25-MAR-2003 (updated)

DT 15-FEB-1995 (first entry)

XX

DE Antisense oligonucleotide for mouse POF.

XX

KW Fibroblast growth factor; hybridisation; laser procedures;

KW vascular smooth muscle cell; proliferation;

KW SMC; vascular stenosis; post angioplasty restenosis;

KW atherosclerosis; cardiac hypertrophy; organ transplant; ss.

XX

OS Synthetic.

XX

PN W09415945-A1.

XX

PD 21-JUL-1994.

XX

PF 2

CC hypertrophy, vascular surgery and organ transplant.
 CC See also AA070333-60.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 21 BP; 4 A; 11 C; 2 G; 4 T; 0 other;
 SQ

Query Match 76.7%; Score 13.8; DB 15; Length 21;
 Best Local Similarity 88.2%; Pred. No. 1.5e+04;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGAGGAGGGGCTGGAA 18
 DB 18 GGGATGGGGCTGGAA 2

RESULT 9

AAF96659/C
 ID AAF96659 standard; DNA; 21 BP.

XX AC AAF96659;

XX DT 06-JUN-2001 (first entry)

XX DE Human gene single nucleotide polymorphism #1420.

XX KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
 KW polymorphism; vascular disease; coronary artery disease; forensics;
 KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
 KW pulmonary embolism; paternity test; ds.

XX OS Homo sapiens.

XX EH Key Location/Qualifiers
 FT Variation replace(11,A)
 FT /*tag= a
 FT /standard_name= "single nucleotide polymorphism"

XX PN WO200118250-A2.

XX PD 15-MAR-2001.

XX PF 07-SEP-2000; 2000WO-US24503.

XX PR 10-SEP-1999; 99US-0153357.

XX PR 26-JUL-2000; 2000US-0220947.

XX PR 16-AUG-2000; 2000US-0225724.

XX PA (WHED) WHITEHEAD INST BIOMEDICAL RES.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Lander ES, Gargill M, Ireland JS, Bolik S, Daley GQ, McCarthy JJ;

XX DR WPI; 2001-226749/23.

XX PT Nucleic acids comprising single nucleotide polymorphisms, useful in
 PT applications such as forensics, paternity testing, medicine, genetic
 PT analysis and phenotype correlations to diseases such as diabetes and
 PT atherosclerosis.

XX PS Examples; Page 145; 242pp; English.

XX CC The present invention provides a method of diagnosing a vascular disease
 CC in an individual, involving determining the sequence at various
 CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
 CC genes. The sequences at a number of polymorphic sites are also provided
 CC in the specification. In particular, the method can be used in the
 CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
 CC disease, stroke, peripheral vascular diseases, venous thromboembolism
 CC and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
 CC useful in forensics, paternity testing, genetic analysis and phenotype
 CC correlations to diseases. The present sequence is an example of one of
 CC the human gene SNPs shown in the specification.

SQ Sequence 21 BP; 2 A; 12 C; 2 G; 5 T; 0 other;

Query Match 76.7%; Score 13.8; DB 22; Length 21;
 Best Local Similarity 88.2%; Pred. No. 1.5e+04;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGAGGAGGGGCTGGA 17

DB 21 GGGAGGAGGACGCTGGA 5

RESULT 10

AAZ18648
 ID AAZ18648 standard; DNA; 20 BP.

XX AC AAZ18648;

XX DT 19-OCT-1999 (first entry)

XX DE ASTH1 gene intron/exon junction sequence.

XX KW ASTH1; asthma; human; chromosome 11p; ASTH1; ASTH1J; genetic locus;
 KW therapeutic; immunogen; polymorphism; junction; ss.

XX OS Homo sapiens.

XX PN WO9337809-A1.

XX PD 29-JUL-1999.

XX PF 21-JAN-1998; 98WO-US01260.

XX PR 21-JAN-1998; 98WO-US01260.

XX PA (AXYS-) AXYS PHARM INC.

XX PI Brooks-Wilson AR, Buckler A, Cardon L, Carey AH;

XX PI Galvin M, Miller A, North M;

XX DR WPI; 1999-479058/40.

XX PT Mammalian asthma related genes, useful for diagnosis of a

XX PT predisposition to development of asthma

XX PS Disclosure; Page 57; 195pp; English.

XX CC The invention identifies a genetic locus ASTH1 associated with asthma,
 CC mapped to human chromosome 11p. ASTH1 and ASTH1J are genes present
 CC within the locus, located close to each other on human chromosome 11p,
 CC and have similar patterns of expression, and common sequence motifs. The
 CC ASTH1 genes and fragments, encoded protein, genomic regulatory regions
 CC and anti-ASTH1 antibodies are useful in the identification of
 CC individuals predisposed to development of asthma, and for the modulation
 CC of gene activity in vivo for prophylactic and therapeutic purposes. The
 CC ASTH1 protein is useful as an immunogen to raise specific antibodies, in
 CC drug screening for compositions that mimic or modulate ASTH1 activity or
 CC expression, including altered forms of ASTH1 protein, and as a
 CC therapeutic. Sequences AAZ18643-218685 intron/exon junction sequences of
 CC ASTH1 and ASTH1J genes.

XX SQ Sequence 20 BP; 3 A; 2 C; 12 G; 3 T; 0 other;

Query Match 74.4%; Score 13.4; DB 20; Length 20;
 Best Local Similarity 93.3%; Pred. No. 2.1e+04;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGAGGAGGGGCTG 15

DB 5 GGTGAGGAGGGGCTG 19

RESULT 11

AAA93151

ID AAA93151 standard; DNA; 20 BP.
 AC AAA93151;
 XX
 DT 12-JAN-2001 (first entry)
 DE Clone vql5_1 secreted protein coding sequence probe SEQ ID NO: 82.
 XX
 KW Human secreted protein; cytokine; cell proliferation;
 KW nutritional supplement; immune modulation; autoimmune disorder;
 KW haematopoiesis regulation; tissue growth; haemostasis; inflammation;
 KW probe; ss.
 XX
 OS Homo sapiens.
 PN WO200049134-A1.
 XX
 PD 24-AUG-2000.
 XX
 PF 18-FEB-2000; 2000WO-US04340.
 PR 19-FEB-1999; 99US-0120680.
 PR 23-APR-1999; 99US-0298733.
 PR 17-AUG-1999; 99US-0149639.
 PR 23-SEP-1999; 99US-0155686.
 PR 01-OCT-1999; 99US-0157247.
 PR 29-NOV-1999; 99US-0167822.
 PR 29-NOV-1999; 99US-0167823.
 PR 15-FEB-2000; 2000US-0298733.
 XX
 PA (ALPH-) ALPHAGENE INC.
 XX
 PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;
 XX
 DR WPI; 2000-549267/50.
 XX
 PT New secreted proteins and polynucleotides encoding them, which are
 PT derived from Homo sapiens, useful for therapy, diagnosis, and research,
 PT as well as nutritional sources or supplements -
 XX
 PS Disclosure; Page 294; 309pp; English.
 XX
 CC The present invention is concerned with a number of secreted proteins
 CC and their coding sequences isolated from various human cDNA libraries.
 CC The probes shown in the specification (AAA93132-A93156) can be used to
 CC obtain the cloned sequences from bacterial cells. The proteins and
 CC coding sequences can be used in the isolation of similar genes and
 CC proteins, in the elucidation of their function in vivo, and to treat a
 CC number of conditions. It is possible that they may have uses as
 CC nutritional supplements, as cytokine or cell proliferation factors, in
 CC immune modulation, where they may be used to treat immune and autoimmune
 CC diseases, as haematopoiesis regulators (treating myeloid or lymphoid
 CC cell deficiencies), in the promotion of tissue growth, they may have
 CC chemokine or chemotactic activity, haemostatic or thrombolytic activity,
 CC or anti-inflammatory activity.
 XX
 SQ Sequence 20 BP; 7 A; 1 C; 10 G; 2 T; 0 other;
 Query Match 74.4%; Score 13.4; DB 21; Length 20;
 Best Local Similarity 93.3%; Pred. No. 2.1e+04;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 GGAGGAGGGGCTGGA 17
 |||||
 Db 4 GGAGGAGGGGCTGGA 18
 RESULT 12
 AAA80555
 ID AAA80555 standard; DNA; 20 BP.
 XX
 AC AAA80555;
 XX

DT 22-NOV-2000 (first entry)
 XX
 DE Human ASTH11 gene exon k 5' boundary region.
 XX
 KW ASTH11 locus; ASTH11; human; chromosome 11p; asthma;
 KW bronchial hyperreactivity; ets family; transcription factor;
 KW splice variant; genetic predisposition; polymorphism; antibody;
 KW drug screening; prophylaxis; therapy; diagnosis; exon boundary; ss.
 XX
 OS Homo sapiens.
 PN US6087485-A.
 XX
 PD 11-JUL-2000.
 XX
 PF 21-JAN-1998; 98US-0009913.
 XX
 PR 21-JAN-1997; 97US-0035663.
 PR 01-JUL-1997; 97US-0051432.
 XX
 XX (AXYS-) AXYS PHARM INC.
 PA Galvin M, Millier A, North M, Cardon L, Buckler A;
 PI Brooks-Wilson AR, Carey AH;
 XX
 DR WPI; 2000-505109/45.
 XX
 PT New nucleic acids other than naturally occurring chromosomes encoding
 PT ASTH1 protein, for e.g. screening compositions that modulate expression
 PT or function of ASTH1 proteins or as diagnostics for genetic
 PT predisposition to asthma -
 XX
 PS Examples; Column 37; 131pp; English.
 XX
 CC The invention relates to the ASTH1 locus on the short arm of human
 CC chromosome (11p). This locus comprises the ASTH11 and ASTH1J genes,
 CC which are associated with a genetic predisposition to asthma and
 CC bronchial hyperreactivity. The ASTH11 and ASTH1J genes are oriented in
 CC opposite directions with the ASTH1 locus, and have similar patterns of
 CC expression and common sequence motifs. They are both expressed in
 CC trachea, lung and several other tissues. ASTH11 and ASTH1J are novel
 CC members of the ets family of transcription factors, which have been
 CC implicated in the activation of a variety of genes including the TCRa
 CC gene and cytokine genes known to be important in the aetiology of
 CC asthma. Both ASTH11 and ASTH1J mRNAs are alternatively spliced.
 CC Alternative splicing of transcripts has no effect on the open reading
 CC frame of ASTH1J, as the exons involved are all 5' to the start codon in
 CC exon b. In contrast, alternative splicing of ASTH11 transcripts results
 CC in 3 different ASTH11 isoforms. The invention also encompasses mouse
 CC asth1j protein. The ASTH11 nucleic acids are useful as diagnostics to
 CC identify a hereditary predisposition to asthma, as probes for identifying
 CC ASTH1 related genes, for identifying expression of the gene in a
 CC biological specimen, and for generating genetically modified non-human
 CC animals or site specific gene modifications in cell lines. The encoded
 CC ASTH1 proteins are useful as immunogens to raise specific antibodies; in
 CC drug screening for compositions that mimic or modulate activity or
 CC expression of ASTH11 and/or ASTH1J (including altered forms of these
 CC proteins); and as a therapeutic. The ASTH1 genes or fragments thereof,
 CC encoded proteins, ASTH1 genomic regulatory regions, and anti-ASTH11 and
 CC anti-ASTH1J antibodies are useful in the identification of individuals
 CC predisposed to development of asthma, and for modulation of gene activity
 CC in vivo for prophylactic and therapeutic purposes. The intact ASTH11 or
 CC ASTH1J proteins or active fragments thereof may be used to modulate or
 CC reduce bronchial hyperreactivity. Sequences AAA80550-A80570 represent the
 CC exon boundary regions of the human ASTH11 gene.
 XX
 SQ Sequence 20 BP; 3 A; 2 C; 12 G; 3 T; 0 other;
 Query Match 74.4%; Score 13.4; DB 21; Length 20;
 Best Local Similarity 93.3%; Pred. No. 2.1e+04;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGGGAGGAGGGGCTG 15

Db 5 GGTGAGGAGGGGCTG 19
 RESULT 13
 AAC68417 ID AAC68417 standard; DNA; 21 BP.
 AC AAC68417;
 XX
 DT 21-FEB-2001 (first entry)
 DE Primer #2 used to isolate human ECE-3.
 KW ECE-3; endothelin converting enzyme 3; hypertension;
 KW atherosclerosis; vascular restenosis;
 KW myocardial ischemia; cerebral vasospasm; subarachnoid hemorrhage;
 KW congestive heart failure; diabetes; endotoxemic shock; migraine;
 KW Raynaud's disease; pulmonary disease; ss.
 XX
 OS Synthetic.
 XX
 FN WO200065025-A2.
 XX
 PD 02-NOV-2000.
 XX
 PF 21-APR-2000; 2000WO-US10828.
 XX
 PR 23-APR-1999; 99US-0130691.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Austin CP, Bailey WJ, Ma L;
 XX
 DR WPI; 2000-687323/67.
 XX
 PT Nucleic acid molecule encoding human endothelin converting enzyme-3
 PT protein, useful for screening modulators that are useful for treating
 PT atherosclerosis, myocardial and cerebral ischemia, and diabetes
 XX
 PS Example 1; Page 40; 78pp; English.
 XX
 CC The present invention relates to human endothelin converting
 CC enzyme-3 protein (ECE-3). ECE-3 is useful for screening selective
 CC modulators of vertebrate ECE-3 function, that are useful for treating
 CC diseases such as hypertension, atherosclerosis, vascular restenosis,
 CC myocardial ischemia, cerebral vasospasm and subarachnoid hemorrhage,
 CC congestive heart failure, diabetes, endotoxemic shock, migraine.
 CC Raynaud's disease, and also for treating pulmonary disease such as
 CC asthma, pulmonary hypertension and adult respiratory distress
 CC syndrome.
 XX
 SQ Sequence 21 BP; 3 A; 3 C; 12 G; 3 T; 0 other;
 Query Match 72.2%; Score 13; DB 21; Length 21;
 Best Local Similarity 100.0%; Pred No. 3e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 6 GGAGGGGCTGAA 18
 Db 7 GGAGGGGCTGAA 19
 RESULT 14
 ABK00898/c ID ABK00898 standard; RNA; 17 BP.
 XX
 AC ABK00898;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human NOGO Inozyme #169.
 XX

KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 PN WO200159103-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US04273.
 XX
 PR 11-FEB-2000; 2000US-181797P.
 PR 28-FEB-2000; 2000US-185516P.
 PR 06-MAR-2000; 2000US-187128P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 PI Blatt L, McSwiggen J, Chowrira BM;
 XX
 DR WPI; 2001-607195/69.
 XX
 PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,
 PT and central nervous system injury
 XX
 PS Claim 88; Page 80; 200pp; English.
 XX
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO).
 CC The nucleic acids may be enzymatic nucleic acids (e.g., a ribozyme or a
 CC DNzyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN
 CC motif) or an amberzyme (cleaving RNA with an NGN triplet), a zinzyme
 CC (cleaving RNA with a YGY motif). The CD20-targeting nucleic acid is used
 CC to cleave RNA of CD20 in the presence of a divalent cation that is
 CC preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce
 CC CD20 activity of the cell and treat a patient having a condition
 CC associated with the level of CD20. The treatment may further comprise the
 CC use of one or more therapies. In particular, the CD20 targeting
 CC nucleic acid may be used to treat lymphoma, leukaemia, B-cell
 CC lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky
 CC low-grade or follicular NHL, lymphocytic leukaemia, HIV (human
 CC immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL),
 CC immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune
 CC thrombocytopaenia, and inflammatory arthropathy. The NOGO-targeting
 CC nucleic acid is used to cleave RNA of the NOGO gene in the presence of a
 CC divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid
 CC may be contacted with a cell to reduce NOGO activity of the cell and
 CC treat a patient having a condition associated with the level of NOGO. The
 CC treatment may further comprise the use of one or more therapies.
 CC In particular, the NOGO-targeting nucleic acid may be used to treat
 CC central nervous system (CNS) injury and cerebrovascular accident (CVA,
 CC stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The

CC present sequence is an inozyme of the invention.
 XX Sequence 17 BP; 0 A; 13 C; 1 G; 3 U; 0 other;
 SQ Query Match 71.1%; Score 12.8; DB 23; Length 17;
 Best Local Similarity 87.5%; Pred. No. 3.6e+04;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGG 16
 |||||
 DB 17 GGGGAGGAGGGGAGG 2

RESULT 15
 ID ABK00899/c
 AC ABK00899;
 XX DT 12-MAR-2002 (first entry)
 XX DE Human NOGO Inozyme #169.
 XX KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; neurotrophic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNzyme; inozyme; G-cleaver; amberyne; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jacob disease; muscular dystrophy; neurodegenerative disease.
 XX OS Homo sapiens.
 OS Synthetic.
 XX WO200159103-A2.
 PN 16-AUG-2001.
 PD 09-FEB-2001; 2001WO-US04273.
 PF 11-FEB-2000; 2000US-181797P.
 PR 28-FEB-2000; 2000US-185516P.
 PR 06-MAR-2000; 2000US-187128P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX Blatt L, McSwiggen J, Chowrira BM;
 PI WPI; 2001-607195/69.
 DR Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia,
 PT and central nervous system injury -
 XX Claim 88; Page 80; 200pp; English.

CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO).
 CC The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNzyme) an inozyme (an endolytic nucleic acid cleaving a an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN
 CC motif) pr an amberyne (cleaving RNA with an NGN triplet), a zinzyme
 CC (cleaving RNA with a YGY motif). The CD20-targetting nucleic acid is used

CC to cleave RNA of CD20 in the presence of a divalent cation that is
 CC preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce
 CC CD20 activity of the cell and treat a patient having a condition
 CC associated with the level of CD20. The treatment may further comprise the
 CC use of one or more therapies. In particular, the CD20 targetting
 CC nucleic acid may be used to treat lymphoma, leukaemia, B-cell
 CC lymphoma, low-grade or follicular NHL, lymphocytic leukaemia, HIV (human
 CC immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL),
 CC immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune
 CC thrombocytopenia, and inflammatory arthropathy. The NOGO-targetting
 CC nucleic acid is used to cleave RNA of the NOGO gene in the presence of a
 CC divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid
 CC may be contacted with a cell to reduce NOGO activity of the cell and
 CC treat a patient having a condition associated with the level of NOGO. The
 CC treatment may further comprise the use of one or more therapies.
 CC In particular, the NOGO-targetting nucleic acid may be used to treat
 CC central nervous system (CNS) injury and cerebrovascular accident (CVA,
 CC stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jacob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The
 CC present sequence is an inozyme of the invention.
 XX Sequence 17 BP; 0 A; 14 C; 0 G; 3 U; 0 other;
 SQ Query Match 71.1%; Score 12.8; DB 23; Length 17;
 Best Local Similarity 87.5%; Pred. No. 3.6e+04;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGG 16
 |||||
 DB 16 GGGGAGGAGGGGAGG 1

Search completed: October 27, 2003, 11:25:19
 Job time : 163 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:29 ; Search time 1581.77 Seconds
(without alignments)
276.576 Million cell updates/sec

Title: US-09-331-204A-5

Perfect score: 18

Sequence: 1 gggaggagggtggaa 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2781392 segs, 12152238056 residues

Total number of hits satisfying chosen parameters: 11152

Minimum DB seq length: 0

Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estmu.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_hci.*

9: gb_estl.*

10: gb_est2.*

11: gb_hci.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_estom.*

17: em_gss_hum.*

18: em_gss_inv.*

19: em_gss_pln.*

20: em_gss_vrt.*

21: em_gss_fun.*

22: em_gss_mam.*

23: em_gss_mus.*

24: em_gss_pro.*

25: em_gss_rod.*

26: em_gss_phg.*

27: em_gss_vrl.*

28: gb_gssi.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12.4	68.9	22	28	AZ307952 1M0010L24
2	12	66.7	16	9	A968729 or69h11.s
3	12	66.7	21	9	AU254493
4	11.8	65.6	19	9	A1696833 wc74e09.x

5	11.8	65.6	20	28	AZ579495	1M03167C13
6	11.6	64.4	21	28	AZ512534	1M03158B07
7	11.4	63.3	19	28	AZ4345792	1M0080G12
8	11.2	62.2	20	28	AZ493581	1M0328A24
9	11.2	62.2	20	28	AZ512326	1M03157118
10	11.2	62.2	20	28	AZ645269	1M0510B10
11	11.2	62.2	20	28	AZ772707	1M0583118
12	11.2	62.2	20	28	AZ969440	1M0242012
13	11.2	62.2	21	28	AZ433710	1M0219P12
14	11.2	62.2	21	28	AZ476392	1M0298F12
15	11.2	62.2	21	28	AZ493585	1M0333H02
16	11.2	62.2	21	28	AZ583408	1M0378N23
17	11.2	62.2	21	28	AZ653464	1M0527G11
18	11.2	62.2	21	28	AZ871715	1M0184B13
19	11.2	62.2	22	28	AZ331988	1M0060B11
20	11.2	62.2	22	28	AZ607348	1M0429D18
21	11.2	62.2	22	28	AZ645874	1M0511C07
22	11.2	62.2	22	28	AZ805739	2M0067K14
23	11.2	62.2	22	28	AZ861868	2M0168L19
24	11.2	62.2	22	28	AZ871408	2M0184E16
25	11	61.1	21	28	AZ967090	1M0237D24
26	10.8	60.0	19	28	AZ326174	1M0048A07
27	10.8	60.0	20	28	AZ405596	1M0174B06
28	10.8	60.0	21	28	AZ836049	2M0130E11
29	10.6	58.9	19	9	A1702520	cz63G05.X
30	10.6	58.9	19	28	AZ493714	1M0328I04
31	10.6	58.9	19	28	AZ775540	2M0008H15
32	10.6	58.9	20	28	AZ623037	1M0460K16
33	10.6	58.9	20	28	AZ659755	1M0537F22
34	10.6	58.9	21	28	AZ321746	1M0042N20
35	10.6	58.9	21	28	AZ419284	1M0195A16
36	10.6	58.9	21	28	AZ467734	1M0279N18
37	10.6	58.9	21	28	AZ499846	1M0337E23
38	10.6	58.9	21	28	AZ657144	1M0533E12
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ALIGNMENTS

RESULT 1

AZ307952

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AZ307952 22 bp DNA linear GSS 29-SEP-2000
1M0010L24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0010L24 F, genomic survey sequence.

AZ307952.1 GI:10347459

GSS.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 22)

Dunn,D., Aoyagi,A., Barber,M., Becorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.

and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0010 row: 1 column: 24
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 Class: plasmid ends
 High quality sequence stop: 22.
 Location/Qualifiers
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FEATURES

source

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/clone_lib="Mouse 10kb plasmid UUGCLM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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BASE COUNT 5 a 0 c 14 g 3 t

ORIGIN

Query Match 68.9%; Score 12.4; DB 28; Length 22;
 Best Local Similarity 92.9%; Pred. No. 7.9e+05; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 Db 4 GGAGGAGGGGCTGG 17

RESULT 2

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 DEFINITION similar to SW:PRPE HUMAN P02811 BASIC PROLINE-RICH PEPTIDE P-E
 ;contains element MSRI repetitive element ; mRNA sequence.

ACCESSION AA968729.1 GI:13143909
 VERSION EST.
 KEYWORDS Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 16)
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 JOURNAL NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

UNPUBLISHED
 CONTACT: Robert Strausberg, Ph.D.
 EMAIL: cgaps-remail.nih.gov
 TISSUE Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
 www.bio.llnl.gov/bbrp/image/image.html

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 Location/Qualifiers

FEATURES

source

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oligo(dT) primer. Double-stranded cDNA was ligated to Eco  

RI adaptors (Pharmacia), digested with Not I and cloned  

into the Not I and Eco RI sites of the modified pT73  

vector. Library is not normalized. Library was  

constructed by Bento Soares and M. Fatima Bonaldo."

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BASE COUNT 2 a 1 c 13 g 0 t

ORIGIN

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 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 4 GGGGAGGAGGGG 15

RESULT 3

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 DEFINITION BED0002246 3', mRNA sequence.
 ACCESSION AU254493
 VERSION AU254493.1 GI:20316325
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 21)
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 TITLE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 JOURNAL Unpublished
 COMMENT Contact: Kikuya Kato
 Graduate School of Biological Sciences
 Nara Institute of Science and Technology
 8916-5 Takayama, Ikoma, Nara 630-0101, Japan
 Tel: 81-743-72-5581
 Fax: 81-743-72-5589
 Email: kkat@bs.aist-nara.ac.jp/BED/index.html.
 URL: http://love2.aist-nara.ac.jp/BED/index.html.

REFERENCE 1 (bases 1 to 21)
 AUTHORS Kato, K. and Matoba, R.
 TITLE Generation of expressed sequence tags from mouse brain
 JOURNAL Unpublished
 COMMENT Contact: Kikuya Kato
 Graduate School of Biological Sciences
 Nara Institute of Science and Technology
 8916-5 Takayama, Ikoma, Nara 630-0101, Japan
 Tel: 81-743-72-5581
 Fax: 81-743-72-5589
 Email: kkat@bs.aist-nara.ac.jp/BED/index.html.
 URL: http://love2.aist-nara.ac.jp/BED/index.html.

UNPUBLISHED
 CONTACT: Kikuya Kato
 Graduate School of Biological Sciences
 Nara Institute of Science and Technology
 8916-5 Takayama, Ikoma, Nara 630-0101, Japan
 Tel: 81-743-72-5581
 Fax: 81-743-72-5589
 Email: kkat@bs.aist-nara.ac.jp/BED/index.html.
 URL: http://love2.aist-nara.ac.jp/BED/index.html.

FEATURES

source

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ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)

REFERENCE
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
and Wright, D., Weiss, R., 2003. Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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High quality sequence stop: 21.
Location/Qualifiers
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FEATURES
source

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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (G14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 2 a 18 c 0 g 1 t
ORIGIN
Query Match 64.4%; Score 11.6; DB 28; Length 21;
Best Local Similarity 77.8%; Pred. No. 1.5e-06;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GGGGAGGAGGGGTGGAA 18
|||||
Db 21 GGGGAGGAGGGGTGGGA 4

RESULT 7
AZ345792
LOCUS
DEFINITION
1M0080G12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0080G12 R, genomic survey sequence.
ACCESSION
AZ345792
VERSION
GSS.
KEYWORDS
Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)

REFERENCE
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
and Wright, D., Weiss, R., 2003. Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: G column: 12
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1..19

FEATURES
source

1..19
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0080G12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (G14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 1 a 1 c 17 g 0 t
ORIGIN
Query Match 63.3%; Score 11.4; DB 28; Length 19;
Best Local Similarity 92.3%; Pred. No. 1.7e+06;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGGGAGGAGGGGC 13
|||||
Db 6 GGGGAGGAGGGGC 18

RESULT 8
AZ493581/c
LOCUS
DEFINITION
1M0328A24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0328A24 F, genomic survey sequence.
ACCESSION
AZ493581
VERSION
GSS.
KEYWORDS
GSS.

SOURCE
ORGANISM Mus musculus (house mouse)
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0328 row: A column: 24
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.
FEATURES
 Location/Qualifiers
 1..19
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 /clone="UUGC1M0328A24"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
 BASE COUNT 0 a 18 c 1 g 0 t
 ORIGIN
 Query Match 62.2%; Score 11.2; DB 28; Length 19;
 Best Local Similarity 81.2%; Pred. No. 2e+06; 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GGGAGAGGCGGCTGG 16
 ||||| ||||| |||||
 Db 19 GGGGGGGGGGGCGGG 4
 ||||| ||||| |||||
RESULT 9
LOCUS AZ512326/c
DEFINITION 1M035718r Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M035718 R, genomic survey sequence.
ACCESSION AZ512326
VERSION AZ512326.1 GI:10693642

SOURCE
ORGANISM Mus musculus (house mouse)
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0357 row: I column: 18
 Seq primer: CACACAGGAAACAGGTATGACC
 Class: plasmid ends
 High quality sequence stop: 20.
FEATURES
 Location/Qualifiers
 1..20
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M035718"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
 BASE COUNT 0 a 18 c 0 g 2 t
 ORIGIN
 Query Match 62.2%; Score 11.2; DB 28; Length 20;
 Best Local Similarity 81.2%; Pred. No. 2e+06; 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GGGAGAGGCGGCTGG 16
 ||||| ||||| |||||
 Db 20 GGGAGGCGGGGGGGG 5
 ||||| ||||| |||||
RESULT 10
LOCUS AZ645269/c
DEFINITION 1M0510810R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0510810 R, genomic survey sequence.
ACCESSION AZ645269

```

VERSION      AZ645269.1  GI:11774602
KEYWORDS     Mus musculus (house mouse)
SOURCE       Mus musculus
ORGANISM     Mus musculus (house mouse)

REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 20)
              Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
              ,M., Rose,M., Stokes,R., Tingey,A., von Niederhausern,A.
              and Wright,D. Weiss,R.
              Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
              Unpublished
              JOURNAL
              COMMENT
              Contact: Robert B. Weiss
              University of Utah Genome Center
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0510 row: B column: 10
              Seq primer: CACACAGGAACAGCTATGACC
              Class: plasmid ends
              High quality sequence stop: 20.
              Location/Qualifiers
                1..20
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                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGCLM0510B10"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGCLM library"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adaptor DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWD42 (G14732114|9b|AF129072.1), a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adaptor mouse DNA was annealed to
              adaptor vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."
              BASE COUNT      0 a      19 c      0 g      1 t
              ORIGIN
              Query Match      62.2%; Score 11.2; DB 28; Length 20;
              Best Local Similarity 81.2%; Pred. No. 2e+06;
              Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

              Qy      1 GGGGAGGAGGGGCTGG 16
              Db      19 GGGGAGGAGGGGGGGG 4

              RESULT 11
              AZ772707/c
              LOCUS      20 bp      DNA      linear      GSS 16-FEB-2001
              DEFINITION  1M0583L18R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
              clone UUGCLM0583L18 R, genomic survey sequence.

```

```

ACCESSION    AZ772707
VERSION      AZ772707.1  GI:12896303
KEYWORDS     Mus musculus
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus (house mouse)

REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 20)
              Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
              ,M., Rose,M., Stokes,R., Tingey,A., von Niederhausern,A.
              and Wright,D. Weiss,R.
              Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
              Unpublished
              JOURNAL
              COMMENT
              Contact: Robert B. Weiss
              University of Utah Genome Center
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0583 row: L column: 18
              Seq primer: CACACAGGAACAGCTATGACC
              Class: plasmid ends
              High quality sequence stop: 20.
              Location/Qualifiers
                1..20
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                /strain="C57BL/6J"
                /db_xref="taxon:10090"
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                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGCLM library"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adaptor DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWD42 (G14732114|9b|AF129072.1), a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adaptor mouse DNA was annealed to
              adaptor vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."
              BASE COUNT      0 a      19 c      0 g      1 t
              ORIGIN
              Query Match      62.2%; Score 11.2; DB 28; Length 20;
              Best Local Similarity 81.2%; Pred. No. 2e+06;
              Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

              Qy      1 GGGGAGGAGGGGCTGG 16
              Db      18 GGGGAGGAGGGGGGGG 3

              RESULT 12
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              LOCUS      20 bp      DNA      linear      GSS 27-APR-2001
              DEFINITION  2M0242012F Mouse 10kb plasmid UUGCLM library Mus musculus genomic

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clone UUGC2M0242012 F, genomic survey sequence.
 AZ969440 1 GI:13840667
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 20)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112 USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0242 row: 0 column: 12
 Seq primer: CGTTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers
 1..20
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 /clone="UUGC2M0242012"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC2M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (female) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."
 0 a 19 c 0 g 1 t

FEATURES
 source

BASE COUNT
 ORIGIN
 Query Match 62.2%; Score 11.2; DB 28; Length 20;
 Best Local Similarity 81.2%; Pred. No. 2e+06;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GGGGAGGAGGGGGCTGG 16
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 Db 18 GGGGAGGAGGGGGGGGG 3
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 RESULT 13
 AZ433710/c
 LOCUS
 21 bp DNA linear GSS 03-OCT-2000
 AZ433710

DEFINITION
 1M0219P12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0219P12 R, genomic survey sequence.
 AZ433710
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 21)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112 USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0219 row: 0 column: 12
 Seq primer: CACACAGGAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers
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 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."
 0 a 20 c 1 g 0 t

FEATURES
 source

BASE COUNT
 ORIGIN
 Query Match 62.2%; Score 11.2; DB 28; Length 21;
 Best Local Similarity 81.2%; Pred. No. 2e+06;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GGGGAGGAGGGGGCTGG 16
 ||||| ||||| ||||| |||||
 Db 17 GGGGAGGAGGGGGGGGG 2
 ||||| ||||| ||||| |||||
 RESULT 14
 AZ476392/c

LOCUS AZ476392 21 bp DNA linear GSS 04-OCT-2000
 DEFINITION 1M0295F12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0295F12 F, genomic survey sequence.

ACCESSION AZ476392
 VERSION AZ476392.1 GI:10634517
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mamoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

TEL: 801 585 5606
 FAX: 801 585 7177
 EMAIL: ddunn@genetics.utah.edu
 INSERT LENGTH: 10000 Std Error: 0.00
 PLATE: 0295 row: F column: 12
 SEQ PRIMER: CGTTGTAACGACGGCCAGT
 CLASS: plasmid ends
 HIGH QUALITY SEQUENCE STOP: 21.

FEATURES
 Location/Qualifiers
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
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 /sex="Male"
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 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: FWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 0 a 20 c 0 g 1 t
 ORIGIN

Query Match 62.2%; Score 11.2; DB 28; Length 21;
 Best Local Similarity 81.2%; Pred. No. 2e+06;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGGAGGAGGGGCTGG 16
 |||||
 Db 20 GGGGAGGAGGGGCGGG 5

RESULT 15

LOCUS AZ495585/c 21 bp DNA linear GSS 05-OCT-2000
 DEFINITION 1M0331H02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0331H02 R, genomic survey sequence.

ACCESSION AZ495585
 VERSION AZ495585.1 GI:10671122
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mamoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

TEL: 801 585 5606
 FAX: 801 585 7177
 EMAIL: ddunn@genetics.utah.edu
 INSERT LENGTH: 10000 Std Error: 0.00
 PLATE: 0331 row: H column: 02
 SEQ PRIMER: CACACAGGAACAGCTATGACC
 CLASS: plasmid ends
 HIGH QUALITY SEQUENCE STOP: 21.

FEATURES
 Location/Qualifiers
 1..21
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0331H02"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: FWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 2 a 16 c 1 g 2 t
 ORIGIN

Query Match 62.2%; Score 11.2; DB 28; Length 21;
 Best Local Similarity 81.2%; Pred. No. 2e+06;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGGAGGAGGGGCTGG 16
 |||||
 Db 21 GGGGTGGGGGGCGGG 6

Tue Oct 28 17:07:58 2003

us-09-331-204a-5.szlm22.rst

Page 9

Search completed: October 27, 2003, 13:59:24
Job time : 1583.77 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:34 ; Search time 41.3143 Seconds
(without alignments)
192.304 Million cell updates/sec

Title: US-09-331-204A-5

Perfect score: 18

Sequence: 1 GGGAGGAGGCGCTGGAA 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 376294

Minimum DB seq length: 0

Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA.*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*

6: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	13.8	76.7	18	5	PCT-US93-12600-11
C 3	13.8	76.7	21	5	PCT-US93-12600-10
C 4	13.8	76.7	21	5	PCT-US93-12600-13
C 5	13.4	74.4	20	3	US-09-009-913-298
C 6	12.8	71.1	20	1	US-08-250-886A-21
C 7	12.8	71.1	20	2	US-08-468-037A-9
C 8	12.8	71.1	20	2	US-08-471-973A-9
C 9	12.8	71.1	20	2	US-08-756-806A-21
C 10	12.8	71.1	20	2	US-08-465-880-9
C 11	12.8	71.1	20	3	US-09-035-357-9
C 12	12.8	71.1	20	3	US-09-143-214-21
C 13	12.8	71.1	20	3	US-09-000-136-7
C 14	12.8	71.1	20	4	US-09-135-202-9
C 15	12.8	71.1	20	4	US-09-506-073-21
C 16	12.8	71.1	20	4	US-08-803-331-9
C 17	12.8	71.1	20	4	US-09-389-283-9
C 18	12.8	71.1	20	5	PCT-US95-07111A-21
C 19	12.8	71.1	22	4	US-08-337-120A-27
C 20	12.4	68.9	20	4	US-09-659-791A-48
C 21	12.4	68.9	20	4	US-09-659-791A-49
C 22	12.2	67.8	18	5	PCT-US93-12600-26
C 23	12.2	67.8	20	1	US-08-290-936-6
C 24	12.2	67.8	20	2	US-08-343-443B-126
C 25	12.2	67.8	21	5	PCT-US93-12600-19
C 26	12.2	67.8	21	5	PCT-US93-12600-25
C 27	12	66.7	16	1	US-08-152-313-15

C 28	12	66.7	16	1	US-08-579-223-15	Sequence 15, Appl
C 29	12	66.7	16	5	PCT-US94-12947A-15	Sequence 15, Appl
C 30	12	66.7	17	2	US-08-173-489C-127	Sequence 127, App
C 31	12	66.7	21	2	US-08-859-998-128	Sequence 128, App
C 32	12	66.7	21	4	US-09-225-928-128	Sequence 128, App
C 33	12	66.7	21	4	US-09-225-201B-128	Sequence 2, Appl
C 34	11.8	65.6	15	3	US-08-557-210A-2	Sequence 12, Appl
C 35	11.8	65.6	15	5	PCT-US93-12600-12	Sequence 17, Appl
C 36	11.8	65.6	18	5	PCT-US93-12600-17	Sequence 68, Appl
C 37	11.8	65.6	20	1	US-07-977-284A-68	Sequence 5, Appl
C 38	11.8	65.6	20	1	US-08-483-122-5	Sequence 5, Appl
C 39	11.8	65.6	20	1	US-08-483-122-6	Sequence 5, Appl
C 40	11.8	65.6	20	2	US-08-486-648-6	Sequence 6, Appl
C 41	11.8	65.6	20	2	US-08-486-648-6	Sequence 68, Appl
C 42	11.8	65.6	20	2	US-08-256-426B-68	Sequence 5, Appl
C 43	11.8	65.6	20	2	US-08-486-307-5	Sequence 5, Appl
C 44	11.8	65.6	20	2	US-08-486-307-5	Sequence 25, Appl
C 45	11.8	65.6	20	3	US-09-357-070-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1

US-08-173-489C-128/c
; Sequence 128, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSER: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect version 5.1
; CURRENT APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 128:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 bases
; TYPE: nucleic acid
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: third strand derived from alpha-1-
; DESCRIPTION: Globin sequence region in Seq ID No. 5861244127
; HYPOTHETICAL: yes
; ANTI-SENSE: no
; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 128 :FROM 1 TO 17

US-08-173-489C-128

Query Match 76.7%; Score 13.8; DB 2; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGGGAGGAGGGCTGGA 17
|||||
DB 17 GGGGAGGAGGGGAGGA 1

RESULT 2

PCT-US93-12600-11/c
; Sequence 11, Application PC/TUS9312600
; GENERAL INFORMATION:
; APPLICANT: Denner, Larry A.
; APPLICANT: Rege, Ajay A.
; APPLICANT: Dixon, Richard A.F.
; TITLE OF INVENTION: ANTISENSE MOLECULES DIRECTED AGAINST A
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR RECEPTOR GENE FAMILY
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore &
; ADDRESSEE: Milnamow, Ltd.
; STREET: 180 North Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12600
FILING DATE: 28-DEC-1993
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/999,706
FILING DATE: December 31, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Katz, Martin L.
REGISTRATION NUMBER: 25,011
TELEPHONE: (312)616-5400
TELEFAX: (312)616-5460
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US93-12600-11

Query Match 76.7%; Score 13.8; DB 5; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 GGGGAGGAGGGCTGGA 18
|||||
DB 18 GGGATGTGGGCTGGAA 2

RESULT 3

PCT-US93-12600-10/c
; Sequence 10, Application PC/TUS9312600
; GENERAL INFORMATION:
; APPLICANT: Denner, Larry A.
; APPLICANT: Rege, Ajay A.
; APPLICANT: Dixon, Richard A.F.
; TITLE OF INVENTION: ANTISENSE MOLECULES DIRECTED AGAINST A
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR RECEPTOR GENE FAMILY

NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Shore &
ADDRESSEE: Milnamow, Ltd.
STREET: 180 North Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12600
FILING DATE: 28-DEC-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/999,706
FILING DATE: December 31, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Katz, Martin L.
REGISTRATION NUMBER: 25,011
TELEPHONE: (312)616-5400
TELEFAX: (312)616-5460
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US93-12600-10

Query Match 76.7%; Score 13.8; DB 5; Length 21;
Best Local Similarity 88.2%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 GGGGAGGAGGGCTGGA 18
|||||
DB 21 GGGATGTGGGCTGGAA 5

RESULT 4

PCT-US93-12600-13/c
; Sequence 13, Application PC/TUS9312600
; GENERAL INFORMATION:
; APPLICANT: Denner, Larry A.
; APPLICANT: Rege, Ajay A.
; APPLICANT: Dixon, Richard A.F.
; TITLE OF INVENTION: ANTISENSE MOLECULES DIRECTED AGAINST A
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR RECEPTOR GENE FAMILY
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore &
; ADDRESSEE: Milnamow, Ltd.
; STREET: 180 North Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12600
FILING DATE: 28-DEC-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/999,706
FILING DATE: December 31, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Katz, Martin L.
REGISTRATION NUMBER: 25,011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)616-5400
TELEFAX: (312)616-5460
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US93-12600-13

Query Match 76.7%; Score 13.8; DB 5; Length 21;
Best Local Similarity 88.2%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGAGGAGGGCTGGA 18
Db 18 GGGATGTGGGCTGGAA 2

RESULT 5
US-09-009-913-298
Sequence 298, Application US/09009913
Patent No. 6087485
GENERAL INFORMATION:
APPLICANT: AYS Pharmaceuticals, Inc.
TITLE OF INVENTION: Asthma Related Genes
NUMBER OF SEQUENCES: 339
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Ave, Suite 200
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,913
FILING DATE: 21-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: SEQ-4P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3231
TELEFAX: 650-327-3231
TELEX:
INFORMATION FOR SEQ ID NO: 298:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-009-913-298

Query Match 74.4%; Score 13.4; DB 3; Length 20;
Best Local Similarity 93.3%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGAGGAGGGGCTG 15
Db 5 GGTGAGGAGGGCTG 19

RESULT 6
US-08-250-856A-21/c
Sequence 21, Application US/08250856A
Patent No. 5563255
GENERAL INFORMATION:
APPLICANT: Monia, Brett P. and Boggs, Russell T.
TITLE OF INVENTION: Antisense Oligonucleotide Modulation
TITLE OF INVENTION: of raf Gene Expression
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Jane Massey Licata
STREET: 210 Lake Drive East, Suite 201
CITY: Cherry Hill
STATE: NJ
COUNTRY: USA
ZIP: 08002
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250,856A
FILING DATE: May 31, 1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0094
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: Yes
US-08-250-856A-21

Query Match 71.1%; Score 12.8; DB 1; Length 20;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGCTGG 16
Db 20 GGGGAGGAGGAGCGG 5

RESULT 7
US-08-468-037A-9/c
Sequence 9, Application US/08468037A
Patent No. 5859221
GENERAL INFORMATION:
APPLICANT: Phillip Dan Cook
APPLICANT: A. Kawasaki
TITLE OF INVENTION: 2'-Modified Oligonucleotides
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859221ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.

```
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468.037A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 835,932
; FILING DATE: 05-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: Yes
US-08-468-037A-9

Query Match 71.1%; Score 12.8; DB 2; Length 20;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGG 16
   |||||
Db 20 GGGGAGGAGGAGCGGG 5

RESULT 8
US-08-471-973A-9/c
; Sequence 9, Application US/08471973A
; Patent No. 5872232
; GENERAL INFORMATION:
; APPLICANT: Phillip Dan Cook
; APPLICANT: Andrew Kawasaki
; TITLE OF INVENTION: Sugar Modified Oligonucleotides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5872232ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471.973A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 835,932
; FILING DATE: 05-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439

; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: Yes
US-08-471-973A-9

Query Match 71.1%; Score 12.8; DB 2; Length 20;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGG 16
   |||||
Db 20 GGGGAGGAGGAGCGGG 5

RESULT 9
US-08-756-806A-21/c
; Sequence 21, Application US/08756806A
; Patent No. 5952229
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P. and Boggs, Russell T.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation
; TITLE OF INVENTION: of raf Gene Expression
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756.806A
; FILING DATE: No. 5952229ember 26, 1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07111
; FILING DATE: May 31, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/250,856
; FILING DATE: May 31, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0200
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 810-1454
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
US-08-756-806A-21

Query Match 71.1%; Score 12.8; DB 2; Length 20;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGG 16
   |||||
Db 20 GGGGAGGAGGAGCGGG 5
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```

RESULT 10
US-08-465-880-9/c
; Sequence 9, Application US/08465880
; Patent No. 5955589
; GENERAL INFORMATION:
; APPLICANT: Philip Dan Cook
; TITLE OF INVENTION: Gapped 2' Modified Oligonucleotides
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5955589ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,880
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 244,993
; FILING DATE: 21-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: Yes
US-08-465-880-9

Query Match 71.1%; Score 12.8; DB 2; Length 20;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGGAGGAGGGGCTGG 16
Db 20 GGGGAGGAGGAGCGGG 5

RESULT 11
US-09-035-357-9/c
; Sequence 9, Application US/09035357
; Patent No. 6005087
; GENERAL INFORMATION:
; APPLICANT: Phillip Dan Cook
; TITLE OF INVENTION: 2'-Modified Oligonucleotides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6005087ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/035,357
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/468,037
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: Yes
US-09-035-357-9

Query Match 71.1%; Score 12.8; DB 3; Length 20;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGGAGGAGGGGCTGG 16
Db 20 GGGGAGGAGGAGCGGG 5

RESULT 12
US-09-143-214-21/c
; Sequence 21, Application US/09143214
; Patent No. 6090626
; GENERAL INFORMATION:
; APPLICANT: Morita, Brett P. and Boggs, Russell T.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation
; TITLE OF INVENTION: of raf Gene Expression
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/143,214
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/756,806
; FILING DATE: No. 6090626ember 26, 1996
; APPLICATION NUMBER: PCT/US95/07111
; FILING DATE: May 31, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/250,856
; FILING DATE: May 31, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISFH-0200
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 810-1454

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INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: Yes
US-09-143-214-21

Query Match 71.1%; Score 12.8; DB 3; Length 20;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGGAGGAGGGCTGG 16
Db 20 GGGGAGGAGGAGCGGG 5

RESULT 13

US-09-000-136-7/c

Sequence 7, Application US/09000136

Patent No. 6096720

GENERAL INFORMATION:

APPLICANT: Love, William G

APPLICANT: Sharman, Thomas

APPLICANT: Phillips, Judith A

APPLICANT: Nicklin, Paul L

APPLICANT: Hamilton, Karen O

TITLE OF INVENTION: Liposomal Oligonucleotide Compositions

FILE REFERENCE: 4-20536/A/MA 2112

CURRENT APPLICATION NUMBER: US/09/000,136

CURRENT FILING DATE: 1998-04-23

EARLIER APPLICATION NUMBER: GB 9515743.4

EARLIER FILING DATE: 1995-08-01

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PatenIn Ver. 2.0

SEQ ID NO 7

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: oligonucleotide

FEATURE:

OTHER INFORMATION: phosphorothioate backbone

FEATURE:

OTHER INFORMATION: alternative oligonucleotide with uniform

OTHER INFORMATION: phosphorothioate backbone with nucleotides 10-20

OTHER INFORMATION: being substituted by methoxy at the 2' position of

OTHER INFORMATION: the sugar moiety

US-09-000-136-7

Query Match 71.1%; Score 12.8; DB 3; Length 20;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGGAGGAGGGCTGG 16
Db 20 GGGGAGGAGGAGCGGG 5

RESULT 14

US-09-135-202-9/c

Sequence 9, Application US/09135202

Patent No. 6399754

GENERAL INFORMATION:

APPLICANT: Phillip Dan Cook

APPLICANT: Andrew Kawasaki

TITLE OF INVENTION: Sugar Modified Oligonucleotides

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 6399754ris

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/135,202
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/471,973
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Joseph Lucci
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: ISIS-2005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: yes
US-09-135-202-9

Query Match 71.1%; Score 12.8; DB 4; Length 20;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGGAGGAGGGCTGG 16
Db 20 GGGGAGGAGGAGCGGG 5

RESULT 15

US-09-506-073-21/c

Sequence 21, Application US/09506073

Patent No. 6410518

GENERAL INFORMATION:

APPLICANT: Monia, Brett P.

TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/09/506,073

CURRENT FILING DATE: 2000-02-18

EARLIER APPLICATION NUMBER: US 09/143,214

EARLIER FILING DATE: 1998-08-28

EARLIER APPLICATION NUMBER: PCT/US98/13961

EARLIER FILING DATE: 1998-07-06

EARLIER APPLICATION NUMBER: US 08/888,982

EARLIER FILING DATE: 1997-07-07

EARLIER APPLICATION NUMBER: US 08/756,806

EARLIER FILING DATE: 1996-11-26

EARLIER APPLICATION NUMBER: PCT/US95/07111

EARLIER FILING DATE: 1995-05-31

EARLIER APPLICATION NUMBER: US 08/250,856

EARLIER FILING DATE: 1994-05-31

NUMBER OF SEQ ID NOS: 130

SEQ ID NO 21

LENGTH: 20

TYPE: DNA

ORGANISM: artificial sequence

FEATURE:

OTHER INFORMATION: antisense sequence

US-09-506-073-21

Query Match 71.1%; Score 12.8; DB 4; Length 20;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGAGGAGGGCTGG 16
| | | | | | | | | |
Db 20 GGGAGGAGGGAGGGG 5

Search completed: October 27, 2003, 14:03:34
Job time : 42.3143 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 11:25:34 ; Search time 387.943 Seconds
(without alignments)
124.432 Million cell updates/sec

Title: US-09-331-204A-5
Perfect score: 18
Sequence: 1 gggaggaggctgaa 18
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1792395 seqs, 134090451 residues

Total number of hits satisfying chosen parameters: 408622

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*
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2: /cgn2_6/prodata1/pubpna/PCT_NEW_PUB.seq.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12.8	71.1	17	9	US-09-866-108-7484
2	12.8	71.1	17	9	US-09-866-108-7485
3	12.8	71.1	17	11	US-09-780-533A-898
4	12.8	71.1	17	11	US-09-780-533A-899
5	12.8	71.1	17	12	US-10-133-779-45
6	12.8	71.1	20	11	US-09-996-263-9
7	12.8	71.1	20	12	US-10-352-586-9
8	12.8	71.1	20	14	US-10-057-550-21
9	12.8	71.1	20	14	US-10-173-225B-21
10	12.4	68.9	17	9	US-09-866-108-7486
11	12.4	68.9	17	9	US-09-866-108-7487
12	12.4	68.9	17	12	US-10-061-201-1931
13	12.4	68.9	17	12	US-10-061-201-1932
14	12.4	68.9	17	12	US-10-061-201-1933
15	12.4	68.9	17	12	US-10-061-201-1934
16	12.4	67.8	17	11	US-09-780-533A-2409

c 17	12	66.7	17	11	US-09-780-533A-46	Sequence 46, Appl
c 18	12	66.7	17	11	US-09-780-533A-47	Sequence 47, Appl
c 19	12	66.7	17	11	US-09-780-533A-900	Sequence 900, App
c 20	12	66.7	17	11	US-09-780-533A-901	Sequence 901, App
c 21	12	66.7	17	12	US-10-061-201-1935	Sequence 1935, Ap
c 22	12	66.7	17	12	US-10-061-201-1936	Sequence 1936, Ap
c 23	12	66.7	19	10	US-09-225-904-22	Sequence 22, Appl
c 24	12	66.7	19	12	US-10-167-241-1	Sequence 1, Appl
c 25	12	66.7	19	12	US-10-108-732-14	Sequence 14, Appl
c 26	12	66.7	21	10	US-09-934-060A-11	Sequence 11, Appl
c 27	11.8	65.6	17	9	US-09-866-108-7483	Sequence 7483, Ap
c 28	11.8	65.6	17	9	US-09-866-108-8084	Sequence 8084, Ap
c 29	11.8	65.6	17	9	US-09-866-108-8085	Sequence 8085, Ap
c 30	11.8	65.6	17	9	US-09-866-108-8086	Sequence 8086, Ap
c 31	11.8	65.6	17	10	US-09-864-785-339	Sequence 339, App
c 32	11.8	65.6	17	10	US-09-864-785-340	Sequence 340, App
c 33	11.8	65.6	17	10	US-09-864-785-341	Sequence 341, App
c 34	11.8	65.6	17	11	US-09-780-533A-897	Sequence 897, App
c 35	11.8	65.6	17	11	US-09-780-533A-922	Sequence 922, App
c 36	11.8	65.6	17	11	US-09-780-533A-923	Sequence 923, App
c 37	11.8	65.6	17	11	US-09-780-533A-2415	Sequence 2415, Ap
c 38	11.8	65.6	18	9	US-09-730-617-16	Sequence 16, Appl
c 39	11.8	65.6	19	11	US-09-943-416A-11	Sequence 11, Appl
c 40	11.8	65.6	20	11	US-09-925-911-5	Sequence 5, Appl
c 41	11.8	65.6	20	11	US-09-925-911-6	Sequence 6, Appl
c 42	11.8	65.6	20	14	US-10-199-830-5	Sequence 5, Appl
c 43	11.8	65.6	20	14	US-10-199-830-6	Sequence 6, Appl
c 44	11.8	65.6	21	14	US-10-219-616-16	Sequence 16, Appl
c 45	11.8	65.6	22	14	US-10-209-372-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1

US-09-866-108-7484
; Sequence 7484, Application US/09866108
; Patent No. US20020048900A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: A60MICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 7484
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7484

Query Match 71.1%; Score 12.8; DB 9; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.5e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCGAGGAGGGCTGGA 17
| | | | | | | | | | | | | | | | | |
Db 2 GCGAGGAGGGCTGGA 17

RESULT 2

US-09-866-108-7485
; Sequence 7485, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEWICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
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; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 7485

; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7485

Query Match 71.1%; Score 12.8; DB 9; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.5e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCGAGGAGGGCTGGA 17
| | | | | | | | | | | | | | | | | |
Db 1 GCGAGGAGGGCTGGA 16

RESULT 3

US-09-780-533A-898/c
; Sequence 898, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH800,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 898
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-898

Query Match 71.1%; Score 12.8; DB 11; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.5e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCGGAGGAGGGCTGG 16
| | | | | | | | | | | | | | | | | |
Db 17 GCGGAGGAGGGGAGG 2

RESULT 4

US-09-780-533A-899/c
; Sequence 899, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH800,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 899
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-899

Query Match 71.1%; Score 12.8; DB 11; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.5e+04;

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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GGGGAGGAGGGCTGG 16
Db 16 GGGGAGGAGGGGAGG 1

RESULT 5
US-10-133-779-45
; Sequence 45, Application US/10133779
; Publication No. US20030165884A1
; GENERAL INFORMATION:
; APPLICANT: Chow, Robert
; APPLICANT: Tonai, Richard
; TITLE OF INVENTION: High Throughput Methods of HLA Typing
; FILE REFERENCE: 020035-000210US
; CURRENT APPLICATION NUMBER: US/10/133,779
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/747,391
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/172,768
; PRIOR FILING DATE: 1999-12-20
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 45
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-133-779-45

Query Match 71.1%; Score 12.8; DB 12; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.5e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 GGAGGAGGGCTCGAA 18
Db 2 GCAGGAGGGCGCGAA 17

RESULT 6
US-09-996-263-9/c
; Sequence 9, Application US/09996263
; Publication No. US20030004325A1
; GENERAL INFORMATION:
; APPLICANT: Phillip Dan Cook
; APPLICANT: Andrew Kawasaki
; TITLE OF INVENTION: Sugar Modified Oligonucleotides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. US20030004325A1
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/996,263
; FILING DATE: 28-Nov. US20030004325A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/471,973
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucchi
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2005
; TELECOMMUNICATION INFORMATION:
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TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-996-263-9

Query Match 71.1%; Score 12.8; DB 11; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GGGGAGGAGGGCTGG 16
Db 20 GGGGAGGAGGAGCGGG 5

RESULT 7
US-10-352-586-9/c
; Sequence 9, Application US/10352586
; Publication No. US20030187240A1
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: 2'-Modified Oligonucleotides
; FILE REFERENCE: ISIS137
; CURRENT APPLICATION NUMBER: US/10/352,586
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 09/389,283
; PRIOR FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-352-586-9

Query Match 71.1%; Score 12.8; DB 12; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GGGGAGGAGGGCTGG 16
Db 20 GGGGAGGAGGAGCGGG 5

RESULT 8
US-10-057-550-21/c
; Sequence 21, Application US/10057550
; Publication No. US20030032607A1
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/057,550
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 09/506,073
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 09/143,214
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: PCT/US98/13961
; PRIOR FILING DATE: 1998-07-06
; PRIOR APPLICATION NUMBER: US 08/888,982
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: US 08/756,806
; PRIOR FILING DATE: 1996-11-26
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; PRIOR APPLICATION NUMBER: PCT/US95/07111
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/250,856
; PRIOR FILING DATE: 1994-05-31
; NUMBER OF SEQ ID NOS: 130
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-10-057-550-21

Query Match 71.1%; Score 12.8; DB 14; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGCTGG 16
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Db 20 GGGGAGGAGGACGGG 5

RESULT 9

US-10-173-225B-21/c
; Sequence 21, Application US/10173225B
; Publication No. US20030119769A1
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
; FILE REFERENCE: ISPH-0665
; CURRENT APPLICATION NUMBER: US/10/173,225B
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 10/057,550
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 09/143,214
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: PCT/US98/13961
; PRIOR FILING DATE: 1998-07-06
; PRIOR APPLICATION NUMBER: US 08/888,982
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: US 08/756,806
; PRIOR FILING DATE: 1996-11-26
; PRIOR APPLICATION NUMBER: PCT/US95/07111
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/250,856
; PRIOR FILING DATE: 1994-05-31
; NUMBER OF SEQ ID NOS: 109
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-10-173-225B-21

Query Match 71.1%; Score 12.8; DB 14; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGCTGG 16
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Db 20 GGGGAGGAGGACGGG 5

RESULT 10

US-09-866-108-7486
; Sequence 7486, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6

; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00659
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7486
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7486

Query Match 68.9%; Score 12.4; DB 9; Length 17;
Best Local Similarity 92.9%; Pred. No. 3.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAGGAGGGCTGGA 17
|||||
Db 2 GAGGAGGGCTGGA 15

RESULT 11

US-09-866-108-7487
; Sequence 7487, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6

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; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/235,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 7487
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7487
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Query Match 68.9%; Score 12.4; DB 9; Length 17;
Best Local Similarity 92.9%; Pred. No. 3.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 4 GAGGAGGGGCTGGA 17
    ||||| |||||
DB 1 GAGGAGGGGCTGGA 14
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RESULT 12
US-10-061-201-1931/c
; Sequence 1931, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
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; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 1931
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-1931
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Query Match 68.9%; Score 12.4; DB 12; Length 17;
Best Local Similarity 92.9%; Pred. No. 3.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 GGGGAGGAGGGGCT 14
    ||||| |||||
DB 17 GGGGAGGAGGGGAT 4
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RESULT 13
US-10-061-201-1932/c
; Sequence 1932, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 1932
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-1932
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Query Match 68.9%; Score 12.4; DB 12; Length 17;
Best Local Similarity 92.9%; Pred. No. 3.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 GGGGAGGAGGGGCT 14
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DB 16 GGGGAGGAGGGGAT 3
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RESULT 14
US-10-061-201-1933/c
; Sequence 1933, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
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; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
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; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 1933
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-1933

Query Match      68.9%; Score 12.4; DB 12; Length 17;
Best Local Similarity 92.9%; Pred. No. 3.7e-04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGGGAGGAGGGGCT 14
      |||||
Db      15 GGGGAGGAGGGGAT 2

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-1934

Query Match      68.9%; Score 12.4; DB 12; Length 17;
Best Local Similarity 92.9%; Pred. No. 3.7e-04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Search completed: October 27, 2003, 19:00:52
Job time : 387.943 secs

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; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 1934
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-1934/c

Sequence 1934, Application US/10061201
Publication No. US20030166229A1
GENERAL INFORMATION:
APPLICANT: Shannon, Mark
TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
FILE REFERENCE: PB0178
CURRENT APPLICATION NUMBER: US/10/061,201
CURRENT FILING DATE: 2002-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 09/864,761
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/328,205
PRIOR FILING DATE: 2001-10-10
NUMBER OF SEQ ID NOS: 4162
SOFTWARE: Aecomica Sequence Listing Engine
SEQ ID NO 1934
LENGTH: 17
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QM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:35 ; Search time 2356.29 Seconds
(without alignments)
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

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Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	18	100.0	18	19	US-09-331-204A-20
4	15.4	85.6	22	50	US-10-310-188-60578

Sequence 2, Appl
Sequence 5, Appl
Sequence 20, Appl
Sequence 60578, A

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C 5 14.4 80.0 16 50 US-10-303-778-3565 Sequence 3565, Ap
C 6 14.4 80.0 17 50 US-10-310-188-5892 Sequence 5892, Ap
C 7 14.4 80.0 16 1 PCT-US02-25943-61140 Sequence 61140, A
C 8 14.4 80.0 17 48 US-10-227-565-61140 Sequence 61140, A
C 9 14.4 80.0 17 50 US-10-310-188-84932 Sequence 84932, A
C 10 14.4 80.0 17 51 US-10-367-832A-61140 Sequence 61140, A
C 11 14.4 80.0 18 50 US-10-310-188-24767 Sequence 24767, A
C 12 14.4 80.0 18 50 US-10-310-188-61077 Sequence 61077, A
C 13 14.4 80.0 18 50 US-10-310-188-61084 Sequence 61084, A
C 14 14.4 80.0 21 50 US-10-310-188-41819 Sequence 41819, A
C 15 14.4 80.0 21 50 US-10-310-188-41829 Sequence 41829, A
C 16 14.4 80.0 21 50 US-10-310-188-41830 Sequence 41830, A
C 17 14.4 80.0 22 50 US-10-303-778-1410 Sequence 1410, Ap
C 18 14.4 80.0 22 50 US-10-310-188-42169 Sequence 42169, A
C 19 14 77.8 20 50 US-10-310-188-18119 Sequence 18119, A
C 20 13.8 76.7 17 50 US-10-303-778-16780 Sequence 16780, A
C 21 13.8 76.7 18 6 US-08-170-096-11 Sequence 11, Appl
C 22 13.8 76.7 18 49 US-10-266-090-38012 Sequence 38012, A
C 23 13.8 76.7 19 1 PCT-US03-07273-12 Sequence 12, Appl
C 24 13.8 76.7 19 1 PCT-US03-07273-165 Sequence 165, Appl
C 25 13.8 76.7 19 2 PCT-US03-07273-12 Sequence 12, Appl
C 26 13.8 76.7 19 2 PCT-US03-07273-165 Sequence 165, Appl
C 27 13.8 76.7 21 6 US-08-170-096-10 Sequence 10, Appl
C 28 13.8 76.7 21 6 US-08-170-096-13 Sequence 13, Appl
C 29 13.8 76.7 21 28 US-09-657-472-1424 Sequence 1424, Ap
C 30 13.8 76.7 21 50 US-10-310-188-39028 Sequence 39028, A
C 31 13.8 76.7 22 50 US-10-310-188-18209 Sequence 18209, A
C 32 13.4 74.4 16 50 US-10-303-778-14517 Sequence 14517, A
C 33 13.4 74.4 17 50 US-10-303-778-1336 Sequence 1336, Ap
C 34 13.4 74.4 18 50 US-10-310-188-84403 Sequence 84403, A
C 35 13.4 74.4 19 50 US-10-310-188-5724 Sequence 5724, Ap
C 36 13.4 74.4 20 1 PCT-US00-04340-82 Sequence 82, Appl
C 37 13.4 74.4 20 1 PCT-US98-01260-298 Sequence 298, Appl
C 38 13.4 74.4 20 2 PCT-US00-04340-82 Sequence 82, Appl
C 39 13.4 74.4 20 2 PCT-US98-01260-298 Sequence 298, Appl
C 40 13.4 74.4 20 22 US-09-507-209-82 Sequence 82, Appl
C 41 13.4 74.4 20 22 US-09-511-446-298 Sequence 298, Appl
C 42 13.4 74.4 20 49 US-10-266-090-45537 Sequence 45537, A
C 43 13.4 74.4 20 50 US-10-303-778-5139 Sequence 5139, Ap
C 44 13.4 74.4 20 50 US-10-310-188-86072 Sequence 86072, A
C 45 13.4 74.4 21 50 US-10-310-188-18091 Sequence 18091, A

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ALIGNMENTS

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RESULT 1
US-09-331-204-2
; Sequence 2, Application US/09331204
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert
; TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN
; FILE REFERENCE: ICNSequence
; CURRENT APPLICATION NUMBER: US/09/331,204
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US97/23927
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: An oligomer
; OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic
; OTHER INFORMATION: acid. This term includes oligomers consisting of
; OTHER INFORMATION: naturally occurring bases, sugars and intersugar
US-09-331-204-2
Query Match 100.0%; Score 18; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGAGGAGGGGCTGGAA 18
Db 1 GGGGAGGAGGGGCTGGAA 18
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US-09-331-204A-5
; Sequence 5, Application US/09331204A
; GENERAL INFORMATION:
; APPLICANT: ICN Pharmaceuticals, Inc.
; APPLICANT: Tam, Robert
; TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Res
; FILE REFERENCE: 216/013-US1
; CURRENT APPLICATION NUMBER: US/09/331,204A
; CURRENT FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US97/23927
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 18
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-331-204A-5
Query Match 100.0%; Score 18; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGAGGAGGGGCTGGAA 18
Db 1 GGGGAGGAGGGGCTGGAA 18
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US-09-331-204A-20/c
; Sequence 20, Application US/09331204A
; GENERAL INFORMATION:
; APPLICANT: ICN Pharmaceuticals, Inc.
; APPLICANT: Tam, Robert
; TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Res
; FILE REFERENCE: 216/013-US1
; CURRENT APPLICATION NUMBER: US/09/331,204A
; CURRENT FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US97/23927
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 18
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-331-204A-20
Query Match 100.0%; Score 18; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGAGGAGGGGCTGGAA 18
Db 18 GGGGAGGAGGGGCTGGAA 1
RESULT 4
US-10-310-188-60578
; Sequence 60578, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487

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; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60578
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-60578

Query Match 85.6%; Score 15.4; DB 50; Length 22;
Best Local Similarity 94.1%; Pred. No. 3.6e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGAGGAGGGGCTGGA 17
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Db 1 GGGAGGAGGGGCTGGA 17

RESULT 5

US-10-303-778-3565/c
; Sequence 3565, Application US/10303778
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/10/303,778
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 17608
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3565
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-778-3565

Query Match 80.0%; Score 14.4; DB 50; Length 16;
Best Local Similarity 93.8%; Pred. No. 8.9e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGAGGGGCTGGAA 18
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Db 16 GGAGGAGGGGCTGCA 1

RESULT 6

US-10-310-188-5892/c
; Sequence 5892, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5892
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-5892

Query Match 80.0%; Score 14.4; DB 50; Length 16;
Best Local Similarity 93.8%; Pred. No. 8.9e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGAGGGGCTGGAA 18
|||||
Db 16 GGAGGAGGGGCTGCA 1

RESULT 7

PCT-US02-25943-61140/c
; Sequence 61140, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 61140
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (5963161)...(5963177)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 6548
PCT-US02-25943-61140

Query Match 80.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 8.9e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGAGGGGCTGGAA 18
|||||
Db 17 GGAGGAGGGGCTGGAA 2

RESULT 8

US-10-227-565-61140/c
; Sequence 61140, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,565
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 61140
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (5963161)...(5963177)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 6548
US-10-227-565-61140

Query Match 80.0%; Score 14.4; DB 48; Length 17;
Best Local Similarity 93.8%; Pred. No. 8.9e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGAGGGGCTGGAA 18
|||||
Db 17 GGAGGAGGGGCTGGAA 2

RESULT 9

US-10-310-188-84932
; Sequence 84932, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84932
; LENGTH: 17
; TYPE: DNA

; ORGANISM: Homo sapiens
US-10-310-188-84932

Query Match 80.0%; Score 14.4; DB 50; Length 17;
Best Local Similarity 93.8%; Pred. No. 8.9e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGAGGAGGGGCTGG 16
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Db 2 GGGAGGAGGGGCTGG 17

RESULT 10

US-10-367-932A-61140/c
; Sequence 61140, Application US/10367932A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeiger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 61140
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (5963161)...(5963177)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectonObjectNumber = 65484
US-10-367-932A-61140

Query Match 80.0%; Score 14.4; DB 51; Length 17;
Best Local Similarity 93.8%; Pred. No. 8.9e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGAGAGGGGCTGGAA 18
| | | | | | | | | | | | | | | | | |
Db 17 GGAGAGGGGCTGGAA 2

RESULT 11

US-10-310-188-24767
; Sequence 24767, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24767
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-24767

Query Match 80.0%; Score 14.4; DB 50; Length 18;
Best Local Similarity 93.8%; Pred. No. 8.9e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGAGGAGGGGCTGG 16
| | | | | | | | | | | | | | | | | |
Db 1 GGGAGGAGGGGCTGG 16

RESULT 12

US-10-310-188-61077
; Sequence 61077, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics

; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61077
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-61077

Query Match 80.0%; Score 14.4; DB 50; Length 18;
Best Local Similarity 93.8%; Pred. No. 8.9e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGAGGAGGGGCTGG 16
| | | | | | | | | | | | | | | | | |
Db 1 GGGAGGAGGGGCTGG 16

RESULT 13

US-10-310-188-61084
; Sequence 61084, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61084
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-61084

Query Match 80.0%; Score 14.4; DB 50; Length 18;
Best Local Similarity 93.8%; Pred. No. 8.9e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGAGGAGGGGCTGG 16
| | | | | | | | | | | | | | | | | |
Db 1 GGGAGGAGGGGCTGG 16

RESULT 14

US-10-310-188-41819
; Sequence 41819, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41819
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-41819

Query Match 80.0%; Score 14.4; DB 50; Length 21;
Best Local Similarity 93.8%; Pred. No. 9e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGAGGAGGGGCTGG 16
| | | | | | | | | | | | | | | | | |

Db 1 GGGGAGGAGGGGTGG 16

RESULT 15

US-10-310-188-41829

; Sequence 41829; Application US/10310188

; GENERAL INFORMATION:

; APPLICANT: RosettaGenomics

; TITLE OF INVENTION: BIOINFORMATICALY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE

; TITLE OF INVENTION: USES THEREOF

; FILE REFERENCE: 47487

; CURRENT APPLICATION NUMBER: US/10/310,188

; CURRENT FILING DATE: 2002-12-19

; NUMBER OF SEQ ID NOS: 86841

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 41829

; LENGTH: 21

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-310-188-41829

Query Match 80.0%; Score 14.4; DB 50; Length 21;

Best Local Similarity 93.8%; Pred.No. 9e+04;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 3 GGGGAGGAGGGGTGG 18

Search completed: October 27, 2003, 17:52:52

Job time : 2357.29 secs


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Db 16 GGAGGAGGGGCTGGCA 1

RESULT 3
PCT-US02-38216-84932
; Sequence 84932, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 84932
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-84932

Query Match      80.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GGGGAGGAGGGGCTGG 16
    |||||
Db 2 GGGGAGGAGGGGCTGG 17

RESULT 4
PCT-US02-38216-24767
; Sequence 24767, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24767
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-24767

Query Match      80.0%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GGGGAGGAGGGGCTGG 16
    |||||
Db 2 GGGGAGGAGGGGCTGG 17

RESULT 5
PCT-US02-38216-61077
; Sequence 61077, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61077
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-61077

Query Match      80.0%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GGGGAGGAGGGGCTGG 16
    |||||
Db 1 GGGCAGGAGGGGCTGG 16

RESULT 6
PCT-US02-38216-61084
; Sequence 61084, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61084
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-61084

Query Match      80.0%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GGGGAGGAGGGGCTGG 16
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Db 1 GGGGAGGAGGGGCTGG 16

RESULT 7
PCT-US02-38216-41819
; Sequence 41819, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41819
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-41819

Query Match      80.0%; Score 14.4; DB 1; Length 21;
Best Local Similarity 93.8%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GGGGAGGAGGGGCTGG 16
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Db 1 GGGGAGGAGGGGCTGG 16

RESULT 8
PCT-US02-38216-41829
; Sequence 41829, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
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; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41829
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-41829

Query Match 80.0%; Score 14.4; DB 1; Length 21;
Best Local Similarity 93.8%; Pred. No. 1e+04; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1

Qy 1 GGGGAGGAGGGGCTGG 16
| | | | | | | | | | | | | | | | | |
Db 3 GGGGAGGAGGGGCTGG 18

RESULT 9
PCT-US02-38216-41830
; Sequence 41830, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41830
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-41830

Query Match 80.0%; Score 14.4; DB 1; Length 21;
Best Local Similarity 93.8%; Pred. No. 1e+04; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1

Qy 1 GGGGAGGAGGGGCTGG 16
| | | | | | | | | | | | | | | | | |
Db 6 GGGGAGGAGGGGCTGG 21

RESULT 10
PCT-US02-38216-42169
; Sequence 42169, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42169
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-42169

Query Match 80.0%; Score 14.4; DB 1; Length 22;
Best Local Similarity 93.8%; Pred. No. 1e+04; 0; Mismatches 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1

Qy 1 GGGGAGGAGGGGCTGG 16
| | | | | | | | | | | | | | | | | |
Db 6 GGGGAGGAGGGGCTGG 21

RESULT 11
PCT-US02-38216-18119
; Sequence 18119, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18119
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-18119

Query Match 77.8%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+04; 0; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0

Qy 3 GGGGAGGAGGGCTGG 16
| | | | | | | | | | | | | | | | | |
Db 1 GGGGAGGAGGGCTGG 14

RESULT 12
PCT-US02-38216-39028
; Sequence 39028, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39028
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-39028

Query Match 76.7%; Score 13.8; DB 1; Length 21;
Best Local Similarity 88.2%; Pred. No. 1.8e+04; 2; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 2

Qy 1 GGGGAGGAGGGCTGGA 17
| | | | | | | | | | | | | | | | | |
Db 5 GAGGAGGAGGGGATGGA 21

RESULT 13
PCT-US02-38216-18209
; Sequence 18209, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18209
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-18209

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Query Match      76.7%; Score 13.8; DB 1; Length 22;
Best Local Similarity 88.2%; Pred. No. 1.8e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGAGGAGGGGCTGGA 17
   |||||
Db 3 GGGGAGGAGGGGAGGA 19

RESULT 14
PCT-US02-38216-84403/c
; Sequence 84403, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 84403
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-84403

Query Match      74.4%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.5e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGAGGGGCTGGA 17
   |||||
Db 18 GGCGGAGGGGCTGGA 4

RESULT 15
PCT-US02-38216-5724
; Sequence 5724, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5724
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-5724

Query Match      74.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 2.5e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGAGGGGCTGGA 17
   |||||
Db 1 GGAGGAGGGGCTGGA 15

Search completed: October 27, 2003, 18:22:55
Job time : 307.029 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:29 ; Search time 438.8 Seconds
(without alignments)
1957.844 Million cell updates/sec

Title: US-09-331-204A-6

Perfect score: 21

Sequence: 1 ggggttgagggggtgggtggg 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 681044

Minimum DB seq length: 0

Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: gb_in.*

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5: gb_ov.*

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7: gb_ph.*

8: gb_pl.*

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14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_on.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

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31: em_htg_inv.*

32: em_htg_oth.*

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34: em_htg_pln.*

35: em_htg_rtd.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_oth.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	18	85.7	18	6	AX023402	Sequence AX023402
2	18	85.7	18	6	AX023427	Sequence AX023427
3	14.2	67.6	20	6	AR078333	Sequence AR078333
4	14.2	67.6	20	6	AR173053	Sequence AR173053
5	14.2	67.6	21	6	AX384817	Sequence AX384817
6	14	66.7	18	6	AX705574	Sequence AX705574
7	14	66.7	18	6	AX705576	Sequence AX705576
8	13.6	64.8	20	6	AR148843	Sequence AR148843
9	13.2	62.9	20	6	AR092032	Sequence AR092032
10	13.2	62.9	20	6	AR112167	Sequence AR112167
11	13.2	62.9	20	6	AR149209	Sequence AR149209
12	13.2	62.9	20	6	AR297674	Sequence AR297674
13	13	61.9	21	6	AR084522	Sequence AR084522
14	13	61.9	21	6	AR084523	Sequence AR084523
15	13	61.9	21	6	AR084559	Sequence AR084559
16	13	61.9	21	6	AR084587	Sequence AR084587
17	13	61.9	21	6	AX023407	Sequence AX023407
18	13	61.9	21	6	121020	Sequence 121020
19	13	61.9	22	6	AR074228	Sequence AR074228
20	13	61.9	22	6	AR074236	Sequence AR074236
21	13	61.9	22	6	AR074302	Sequence AR074302
22	13	61.9	22	6	AR074309	Sequence AR074309
23	13	61.9	22	6	AX032590	Sequence AX032590
24	13	61.9	22	6	AX032598	Sequence AX032598
25	13	61.9	22	6	AX032664	Sequence AX032664
26	13	61.9	22	6	AX032671	Sequence AX032671
27	12.8	61.0	18	6	AR168831	Sequence AR168831
28	12.8	61.0	18	6	AR200300	Sequence AR200300
29	12.8	61.0	18	6	AX262431	Sequence AX262431
30	12.8	61.0	18	6	AX233412	Sequence AX233412
31	12.8	61.0	18	6	E04543	Sequence E04543 linker, 9/1
32	12.8	61.0	19	6	AX659401	Sequence AX659401
33	12.8	61.0	20	6	AR015996	Sequence AR015996
34	12.8	61.0	20	6	AR082037	Sequence AR082037
35	12.8	61.0	20	6	AR126606	Sequence AR126606
36	12.8	61.0	20	6	AR167146	Sequence AR167146
37	12.8	61.0	20	6	AR167147	Sequence AR167147
38	12.8	61.0	21	6	A20477	Sequence A20477 oligonucleo
39	12.8	61.0	21	6	A28676	Sequence A28676 dsRNA with
40	12.8	61.0	21	6	AR061827	Sequence AR061827
41	12.8	61.0	21	6	AR252818	Sequence AR252818
42	12.8	61.0	22	6	BD182437	Sequence BD182437 Human art
43	12.8	61.0	22	6	E38866	Sequence E38866 Chimeric an
44	12.8	61.0	22	6	E63496	Sequence E63496 Non-human a
45	12.6	60.0	19	6	AR128076	Sequence AR128076

ALIGNMENTS

RESULT 1	AX023402	Sequence 17 from Patent WO0014217.	18 bp	DNA	linear	PAT 15-SEP-2000
LOCUS	AX023402	Sequence 17 from Patent WO0014217.				
DEFINITION	AX023402	Sequence 17 from Patent WO0014217.				
ACCESSION	AX023402	Sequence 17 from Patent WO0014217.				
VERSION	AX023402.1	GI:10183802				
KEYWORDS		synthetic construct				
SOURCE		synthetic construct				
ORGANISM		artificial sequences.				
REFERENCE	1	Lipford G. B., Heeg K. and Wagner, H.				
AUTHORS		G-motif oligonucleotides and uses thereof				
TITLE		Patent: WO 0014217-A 17 16-MAR-2000;				
JOURNAL		LIPFORD GRAYSON B (DE) ; HEEG KLAUS (DE) ; WAGNER HERMANN (DE) ;				

CPG IMMUNOPHARMACEUTICALS GMBH (DE)

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/organism="synthetic construct"
/mol_type="genomic DNA"
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/note="synthetic, no natural origin"
BASE COUNT 1 a 0 c 13 g 4 t
ORIGIN

Query Match 85.7%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.9e+03; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;

Qy 4 TTGAGGGGGTGGTGGG 21
Db 1 TTGAGGGGGTGGTGGG 18

RESULT 2
AX023427/c
LOCUS 18 bp DNA linear PAT 15-SEP-2000
DEFINITION Sequence 42 from Patent WO014217.
ACCESSION AX023427
VERSION AX023427.1 GI:10183827
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Lipford,G.B., Heeg,K. and Wagner,H.
TITLE G-motif oligonucleotides and uses thereof
JOURNAL Patent: WO 0014217-A 42 16-MAR-2000;
LIPFORD GRAYSON B (DE); HEEG KLAUS (DE); WAGNER HERMANN (DE);
CPG IMMUNOPHARMACEUTICALS GMBH (DE)
FEATURES
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/mol_type="genomic DNA"
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/note="synthetic, no natural origin"
BASE COUNT 4 a 13 c 0 g 1 t
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Query Match 85.7%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.9e+03; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;

Qy 4 TTGAGGGGGTGGTGGG 21
Db 18 TTGAGGGGGTGGTGGG 1

RESULT 3
AR078333
LOCUS 20 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 2 from patent US 5962426.
ACCESSION AR078333
VERSION AR078333.1 GI:10005079
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)
AUTHORS Glazer,P.M.
TITLE Triple-helix forming oligonucleotides for targeted mutagenesis
JOURNAL Patent: US 5962426-A 2 05-OCT-1999;
FEATURES
source Location/Qualifiers
1. .20
/organism="unknown"
BASE COUNT 3 a 0 c 15 g 2 t
ORIGIN

Query Match 67.6%; Score 14.2; DB 6; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.3e+05; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3;

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Db 2 GGAAGGGGGGGTGGTGGG 20

RESULT 4
AR173053
LOCUS 20 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 2 from patent US 6303376.
ACCESSION AR173053
VERSION AR173053.1 GI:17912544
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)
AUTHORS Glazer,P.M.
TITLE Methods of targeted mutagenesis using triple-helix forming
JOURNAL oligonucleotides
FEATURES Patent: US 6303376-A 2 16-OCT-2001;
source Location/Qualifiers
1. .20
/organism="unknown"
BASE COUNT 3 a 0 c 15 g 2 t
ORIGIN

Query Match 67.6%; Score 14.2; DB 6; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.3e+05; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3;

Qy 2 GGTGGAGGGGGTGGTGGG 20
Db 2 GGAAGGGGGGGTGGTGGG 20

RESULT 5
AX384817
LOCUS 21 bp DNA linear PAT 19-MAR-2002
DEFINITION Sequence 17 from Patent WO0210452.
ACCESSION AX384817
VERSION AX384817.1 GI:19577951
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Chang,C.
TITLE Methods and compositions for predicting prostate cancer
JOURNAL Patent: WO 0210452-A 17 07-FEB-2002;
University of Rochester (US)
FEATURES
source Location/Qualifiers
1. .21
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Sequence can be repeated one or more times"
BASE COUNT 0 a 1 c 15 g 5 t
ORIGIN

Query Match 67.6%; Score 14.2; DB 6; Length 21;
Best Local Similarity 84.2%; Pred. No. 2.3e+05; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3;

Qy 1 GGGTTGGAGGGGGTGGTGG 19
Db 2 GTGGTGGTGGGGGTGGTGG 20

RESULT 6

AX705574
LOCUS AX705574 18 bp DNA linear PAT 04-APR-2003
DEFINITION Sequence 243 from Patent WO03014388.
ACCESSION AX705574
VERSION AX705574.1 GI:29562239
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Distler,J., Model,F. and Taubert,H.
TITLE Method and nucleic acids for the analysis of colon cancer
JOURNAL Patent: WO 03014388-A 243 20-FEB-2003;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Detection oligonucleotide for p16"
BASE COUNT 3 a 0 c 11 g 4 t
ORIGIN
Query Match 66.7%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGTTGGAGGGGGT 14
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Db 5 GGGTTGGAGGGGGT 18
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RESULT 7
AX705576/c
LOCUS AX705576 18 bp DNA linear PAT 04-APR-2003
DEFINITION Sequence 245 from Patent WO03014388.
ACCESSION AX705576
VERSION AX705576.1 GI:29562241
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Distler,J., Model,F. and Taubert,H.
TITLE Method and nucleic acids for the analysis of colon cancer
JOURNAL Patent: WO 03014388-A 245 20-FEB-2003;
FEATURES
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Detection oligonucleotide for p16"
BASE COUNT 4 a 11 c 0 g 3 t
ORIGIN
Query Match 66.7%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGTTGGAGGGGGT 14
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Db 14 GGGTTGGAGGGGGT 1
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RESULT 8
AR148843
LOCUS AR148843 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 204 from patent US 6225451.
ACCESSION AR148843
VERSION AR148843.1 GI:15112933
KEYWORDS Unknown.
SOURCE

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Ballinger,D.G., Ding,W., Wagner,S. and Hess,M.A.
TITLE Chromosome 11-linked coronary heart disease susceptibility gene
JOURNAL CHD1
Patent: US 6225451-A 204 01-MAY-2001;
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/organism="unknown"
BASE COUNT 0 a 1 c 17 g 2 t
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Query Match 64.8%; Score 13.6; DB 6; Length 20;
Best Local Similarity 80.0%; Pred. No. 4e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GGGTTGGAGGGGGTGGTGGG 20
|||||
Db 1 GGGTTGGAGGGGGTGGG 20
|||||
RESULT 9
AR092032/c
LOCUS AR092032 20 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 56 from patent US 5998141.
ACCESSION AR092032
VERSION AR092032.1 GI:10018786
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Acton,S.Laurene.
TITLE Intronic and polymorphic SR-BI nucleic acids and uses therefor
JOURNAL Patent: US 5998141-A 56 07-DEC-1999;
FEATURES
source
1..20
/organism="unknown"
BASE COUNT 4 a 13 c 1 g 2 t
ORIGIN
Query Match 62.9%; Score 13.2; DB 6; Length 20;
Best Local Similarity 83.3%; Pred. No. 5.8e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 GTTGGAGGGGGTGGTGGG 20
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Db 20 GTGGCTGGGGTGGTGGG 3
|||||
RESULT 10
AR112167/c
LOCUS AR112167 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 56 from patent US 6130041.
ACCESSION AR112167
VERSION AR112167.1 GI:14092067
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Acton,S.Laurene.
TITLE Human intronic and polymorphic SR-BI nucleic acids and uses therefor
JOURNAL Patent: US 6130041-A 56 10-OCT-2000;
FEATURES
source
1..20
/organism="unknown"
BASE COUNT 4 a 13 c 1 g 2 t
ORIGIN
Query Match 62.9%; Score 13.2; DB 6; Length 20;

Best Local Similarity 83.3%; Pred. No. 5.8e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GTTGAGGGGGGTGGG 20
Db 20 GTGGGCTGGGTGGG 3

RESULT 11
LOCUS AR149209/c 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 56 from patent US 6228581.
ACCESSION AR149209
VERSION AR149209.1 GI:15113800
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Acton,S.L. and Ordovas,J.M.
TITLE Human intronic and polymorphic SR-BI nucleic acids and uses
JOURNAL Patent: US 6228581-A 56 08-MAY-2001;
FEATURES Location/Qualifiers
source 1..20
BASE COUNT 4 a 13 c 1 g 2 t
ORIGIN

Query Match 62.9%; Score 13.2; DB 6; Length 20;
Best Local Similarity 83.3%; Pred. No. 5.8e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GTTGAGGGGGGTGGG 20
Db 20 GTGGGCTGGGTGGG 3

RESULT 12
LOCUS AR297674/c 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 9409 from patent US 6537751.
ACCESSION AR297674
VERSION AR297674.1 GI:31684958
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 9409 25-MAR-2003;
FEATURES Location/Qualifiers
source 1..20
BASE COUNT 4 a 11 c 0 g 5 t
ORIGIN

Query Match 62.9%; Score 13.2; DB 6; Length 20;
Best Local Similarity 83.3%; Pred. No. 5.8e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGTTGAGGGGGGTGGT 18
Db 20 GAGTTGAGGGGGGATG 3

RESULT 13
LOCUS AR084522/c 21 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 11 from patent US 5981185.
ACCESSION AR084522

Query Match 61.9%; Score 13; DB 6; Length 21;
Best Local Similarity 76.2%; Pred. No. 6.9e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGTTGAGGGGGGTGGG 21
Db 1 GGGGGGGGGGGGGGGGG 21

RESULT 14
LOCUS AR084523 21 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 12 from patent US 5981185.
ACCESSION AR084523
VERSION AR084523.1 GI:10011294
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 12 09-NOV-1999;
FEATURES Location/Qualifiers
source 1..21
BASE COUNT 0 a 0 c 21 g 0 t
ORIGIN

Query Match 61.9%; Score 13; DB 6; Length 21;
Best Local Similarity 76.2%; Pred. No. 6.9e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGTTGAGGGGGGTGGG 21
Db 21 GGGGGGGGGGGGGGGGG 1

RESULT 15
LOCUS AR084559/c 21 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 48 from patent US 5981185.
ACCESSION AR084559
VERSION AR084559.1 GI:10011330
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 48 09-NOV-1999;
FEATURES Location/Qualifiers
source 1..21
BASE COUNT 7 a 14 c 0 g 0 t
ORIGIN

Query Match 61.9%; Score 13; DB 6; Length 21;
Best Local Similarity 76.2%; Pred. NO. 6.9e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGTTGGAGGGGGTGGGG 21
| | | | | | | | | | | | | | | | | | | | |
Db 21 GTGGTGGTGGTGGTGGTG 1

Search completed: October 27, 2003, 11:09:25
Job time : 439.8 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:29 ; Search time 189 Seconds
(without alignments)
299,938 Million cell updates/sec

Title: US-09-331-204A-6

Perfect score: 21

Sequence: 1 ggggtgaggggggtggggg 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 1643890

Minimum DB seq length: 0

Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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24: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*
25: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	21	100.0	21	17	Triplex forming ol
2	21	100.0	21	20	CD28 inhibiting ph
3	21	100.0	21	20	CD28 inhibition ol
4	18	85.7	18	17	Triplex forming ol
5	18	85.7	18	20	CD28 inhibiting ph
6	18	85.7	18	20	CD28 inhibiting ol
7	18	85.7	18	21	Nucleotide sequenc
8	18	85.7	18	21	Nucleotide sequenc

9	16.4	78.1	18	17	AAT36243	CD28 expression in
10	16.4	78.1	18	20	AAX90336	CD28 inhibiting ph
11	14.8	70.5	18	17	AAT36242	CD28 expression in
12	14.8	70.5	18	20	AAT36244	CD28 expression in
13	14.8	70.5	18	20	AAX90335	CD28 inhibiting ph
14	14.8	70.5	18	20	AAX90337	CD28 inhibiting ph
15	14.2	67.6	20	16	AAQ81074	supF gene triplex
16	14.2	67.6	20	18	AAT70012	Triplex-forming ol
17	14.2	67.6	20	18	AAT47061	Oligonucleotide AG
18	14.2	67.6	21	24	AAD30438	Human androgen rec
19	13.6	64.8	20	20	AAZ27025	Apolipoprotein CII
20	13.6	64.8	22	22	AAF16593	Gastric acid produ
21	13.4	63.8	15	24	AAD25952	ASO probe #5 to de
22	13.4	63.8	20	24	ABK89176	Human JAZF1/jjA21
23	13.2	62.9	20	20	AAX24525	Human SR-BI gene e
24	13.2	62.9	20	20	AAX24617	Human SR-BI gene e
25	13.2	62.9	20	21	AAZ75053	Human biallelic ma
26	13.2	62.9	21	17	AAT35046	Triplex-forming ol
27	13.2	62.9	22	20	AAZ22690	STAR (5' sense) pr
28	13	61.9	15	24	ABL39459	Human E7B allele-
29	13	61.9	21	14	AAQ50950	Synthetic oligonuc
30	13	61.9	21	21	AAZ99630	Proteptic blocking
31	13	61.9	21	24	ABK99296	Hepatitis C virus
32	13	61.9	22	15	AAQ61991	Guanine quartet co
33	13	61.9	22	15	AAQ61998	Guanine quartet co
34	13	61.9	22	15	AAQ61995	HSV replication in
35	13	61.9	22	15	AAQ61903	Peptide nucleic ac
36	13	61.9	22	16	AAQ97987	HSV replication in
37	12.8	61.0	16	17	AAT36247	CD28 expression in
38	12.8	61.0	16	20	AAX90340	CD28 inhibiting ph
39	12.8	61.0	17	20	AAV5680	Human tissue kall
40	12.8	61.0	17	21	AAQ01954	Hammerhead ribosym
41	12.8	61.0	17	24	AAZ43484	Human tissue kall
42	12.8	61.0	18	17	AAT36245	CD28 expression in
43	12.8	61.0	18	18	AAT51673	Viral integrase in
44	12.8	61.0	18	19	AAX79255	Oligonucleotide #4
45	12.8	61.0	18	20	AAX90338	CD28 inhibiting ph

ALIGNMENTS

RESULT 1

ID AAT36197 standard; DNA; 21 BP.
XX AAT36197;
XX AAT36197;
XX 25-MAR-2003 (updated)
DT 15-APR-1997 (first entry)
XX
DE Triplex forming oligo targeting CD28 5'-UTR (nt 58-78).

XX Reduction; T cell; CD28; gene expression; treatment; immune system;
KW disorder; graft versus host disease; septic shock; viral disease;
KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;
KW multiple sclerosis; uveitis; rheumatoid arthritis; 5'-UTR;
KW systemic lupus erythematosus; inflammatory bowel disease;
KW triplex forming; oligonucleotide; 5'-untranslated region; ss
XX Synthetic.
XX WO9624380-A1.
PN 15-AUG-1996.
PD 05-FEB-1996;
XX 95WO-US01507.
PF 05-FEB-1996;
XX 95US-0387041.
PR 09-FEB-1995;
XX 95US-0529878.
PR 18-SEP-1995;
XX 95US-0387041.
PR 09-FEB-1995;
XX 95US-0529878.
PR 18-SEP-1995;

PA (ICNC) ICN PHARM INC.
 XX Tam RC;
 XX WPI; 1996-384228/38.
 XX
 PT Oligonucleotide which reduces CD28 gene expression in T cells -
 PT for treating immune system diseases, e.g. graft vs. host disease,
 PT septic shock, psoriasis, etc.
 XX
 XX Claim 10; Page 54; 77pp; English.
 XX
 CC The present oligonucleotide reduces T cell CD28 gene expression,
 CC useful in the treatment of CD28 mediated diseases, particularly
 CC immune system disorders, e.g. graft versus host disease, septic
 CC shock, viral disease, psoriasis, type I diabetes mellitus,
 CC thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid
 CC arthritis, systemic lupus erythematosus, inflammatory bowel
 CC disease, etc.. Reducing CD28 expression may reduce the effects of
 CC antigenic stimulation of CD28 positive T cells, with a consequent
 CC reduction in cytokine release.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX
 XX Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;
 SQ
 Query Match 100.0%; Score 21; DB 17; Length 21;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGGTTGGAGGGGGTGGTGGGG 21
 DB 1 GGGTTGGAGGGGGTGGTGGGG 21
 RESULT 2
 AAX90329
 ID AAX90329 standard; DNA; 21 BP.
 XX
 AC AAX90329;
 XX
 DT 24-SEP-1999 (first entry)
 XX
 XX CD28 inhibiting phosphorothioate oligonucleotide RT04S.
 DE
 XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
 KW immune system mediated disease; gamma-interferon; IL-8;
 KW phosphorothioate; ss.
 XX
 OS Synthetic.
 XX
 PN US5932556-A.
 PD 03-AUG-1999.
 XX
 PF 18-SEP-1995; 95US-0529878.
 XX
 PR 18-SEP-1995; 95US-0529878.
 XX
 PA (TAMR/) TAM R C.
 XX
 PI Tam RC;
 XX
 DR WPI; 1999-443609/37.
 XX
 PT Treatment of immune system-mediated diseases by inhibiting
 PT expression of CD28, IL-2, gamma-interferon or IL-8
 XX
 PS Example; Column 21; 45pp; English.
 XX
 CC The present invention describes a method for inhibiting the expression
 CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
 CC comprises subcutaneous administration of an oligonucleotide (OGN).
 CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
 CC method. The OGNs are used for the treatment of immune system-mediated
 CC diseases.

CC method. The OGNs are used for the treatment of immune system-mediated
 CC diseases. The present sequence represents a CD28 inhibiting
 CC phosphorothioate oligonucleotide used in the exemplification of the
 CC present invention.
 XX
 SQ Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;
 Query Match 100.0%; Score 21; DB 20; Length 21;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGGTTGGAGGGGGTGGTGGGG 21
 DB 1 GGGTTGGAGGGGGTGGTGGGG 21
 RESULT 3
 AAX90291
 ID AAX90291 standard; DNA; 21 BP.
 XX
 AC AAX90291;
 XX
 DT 24-SEP-1999 (first entry)
 XX
 XX CD28 inhibition oligonucleotide RT04.
 DE
 XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
 KW immune system mediated disease; gamma-interferon; IL-8; ss.
 XX
 OS Synthetic.
 XX
 PN US5932556-A.
 PD 03-AUG-1999.
 XX
 PF 18-SEP-1995; 95US-0529878.
 XX
 PR 18-SEP-1995; 95US-0529878.
 XX
 PA (TAMR/) TAM R C.
 XX
 PI Tam RC;
 XX
 DR WPI; 1999-443609/37.
 XX
 PT Treatment of immune system-mediated diseases by inhibiting
 PT expression of CD28, IL-2, gamma-interferon or IL-8
 XX
 PS Claim 6; Column 29; 45pp; English.
 XX
 CC The present invention describes a method for inhibiting the expression
 CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
 CC comprises subcutaneous administration of an oligonucleotide (OGN).
 CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
 CC method. The OGNs are used for the treatment of immune system-mediated
 CC diseases.

```

XX 25-MAR-2003 (updated)
DT 15-APR-1997 (first entry)
XX
XX Triplex forming oligo targetting CD28 5'-UTR (nt 58-75).
XX
XX Reduction; T cell; CD28; gene expression; treatment; immune system;
KW disorder; graft versus host disease; septic shock; viral disease;
KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;
KW multiple sclerosis; uveitis; rheumatoid arthritis; 5'-UTR;
KW systemic lupus erythematosus; inflammatory bowel disease; ss
KW triplex forming; oligonucleotide; 5'-untranslated region; ss
XX
XX Synthetic.
OS
XX WO9624380-A1.
PN
XX
XX 15-AUG-1996.
PD
XX
XX 05-FEB-1996; 96WO-US01507.
PF
XX 09-FEB-1995; 95US-0387041.
PR 18-SEP-1995; 95US-0529878.
PR 09-FEB-1995; 95US-0387041.
PR 18-SEP-1995; 95US-0529878.
XX
XX (ICNC ) ICN PHARM INC.
PA
XX
XX Tam RC;
PI
XX WPI; 1996-384228/38.
XX
XX Oligonucleotide which reduces CD28 gene expression in T cells -
PT for treating immune system diseases, e.g. graft vs. host disease,
PT septic shock, psoriasis, etc.
XX
XX Claim 9; Page 54; 77pp; English.
XX
XX The present oligonucleotide reduces T cell CD28 gene expression,
CC useful in the treatment of CD28 mediated diseases, particularly
CC immune system disorders, e.g. graft versus host disease, septic
CC shock, viral disease, psoriasis, type I diabetes mellitus,
CC thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid
CC arthritis, systemic lupus erythematosus, inflammatory bowel
CC disease, etc. Reducing CD28 expression may reduce the effects of
CC antigenic stimulation of CD28 positive T cells, with a consequent
CC reduction in cytokine release.
CC (Updated on 25-MAR-2003 to correct PR field.)
XX
XX Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;
SQ
Query Match 85.7%; Score 18; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
AAX90328
ID AAX90328 standard; DNA; 18 BP.
XX
XX AAX90328;
AC
XX
XX 24-SEP-1999 (first entry)
DT
XX
XX CD28 inhibiting phosphorothioate oligonucleotide RT03S.
DE
XX
XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
KW immune system mediated disease; gamma-interferon; IL-8;
KW phosphorothioate; ss.

XX 4 TTGAGGGGGTGTGGGG 21
Db 1 TTGAGGGGGTGTGGGG 18

RESULT 6
AAX90290
ID AAX90290 standard; DNA; 18 BP.
XX
XX AAX90290;
AC
XX
XX 24-SEP-1999 (first entry)
DT
XX
XX CD28 inhibition oligonucleotide RT03.
DE
XX
XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
KW immune system mediated disease; gamma-interferon; IL-8; ss.
XX
XX Synthetic.
OS
XX US5932556-A.
PN
XX
XX 03-AUG-1999.
PD
XX
XX 18-SEP-1995; 95US-0529878.
PF
XX 18-SEP-1995; 95US-0529878.
PR
XX (TAMR/) TAM R C.
PA
XX
XX Tam RC;
PI
XX WPI; 1999-443609/37.
XX
XX Treatment of immune system-mediated diseases by inhibiting
PT expression of CD28, IL-2, gamma-interferon or IL-8
XX
XX Example; Column 21; 45pp; English.
XX
XX The present invention describes a method for inhibiting the expression
CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
CC comprises subcutaneous administration of an oligonucleotide (OGN).
CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
CC method. The OGNs are used for the treatment of immune system-mediated
CC diseases. The present sequence represents a CD28 inhibiting
CC phosphorothioate oligonucleotide used in the exemplification of the
CC present invention.
XX
XX Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;
SQ
Query Match 85.7%; Score 18; DB 20; Length 18;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 4 TTGAGGGGGTGTGGGG 21
Db 1 TTGAGGGGGTGTGGGG 18

RESULT 6
AAX90290
ID AAX90290 standard; DNA; 18 BP.
XX
XX AAX90290;
AC
XX
XX 24-SEP-1999 (first entry)
DT
XX
XX CD28 inhibition oligonucleotide RT03.
DE
XX
XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
KW immune system mediated disease; gamma-interferon; IL-8; ss.
XX
XX Synthetic.
OS
XX US5932556-A.
PN
XX
XX 03-AUG-1999.
PD
XX
XX 18-SEP-1995; 95US-0529878.
PF
XX 18-SEP-1995; 95US-0529878.
PR
XX (TAMR/) TAM R C.
PA
XX
XX Tam RC;
PI
XX WPI; 1999-443609/37.
XX
XX Treatment of immune system-mediated diseases by inhibiting
PT expression of CD28, IL-2, gamma-interferon or IL-8

```

XX Claim 5; Column 29; 45pp; English.

XX The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-9 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN), CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the CC method. The OGNs are used for the treatment of immune system-mediated CC diseases.

XX Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;

Query Match 85.7%; Score 18; DB 20; Length 18;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGGAGGGGGTGGTGGGG 21
|||
Db 1 TTGGAGGGGGTGGTGGGG 18

RESULT 7
AAZ99625
ID AAZ99625 standard; DNA; 18 BP.
XX
AC AAZ99625;
XX
DT 12-JUL-2000 (first entry)
XX
DE Nucleotide sequence of G-motif oligonucleotide GRI.

XX G-motif oligonucleotide; vaccine; Toxoplasmosis; viral infection;
KW antigen presenting cell activation; natural killer cell; septic shock;
KW cytotoxic T-lymphocyte; inflammation; autoimmune disease;
KW rheumatoid arthritis; Crohn's disease; sarcoidosis; multiple sclerosis;
KW Kawasaki syndrome; graft-versus-host disease; transplant rejection;
KW helper T cell response 1-mediated disease; Lyme arthritis;
KW Streptococcal induced arthritis; chronic inflammatory bowel disease;
KW psoriasis vulgaris; experimental allergic encephalomyelitis;
KW insulin-dependent diabetes mellitus; bacterial infection;
KW parasitic infection; Leishmaniasis; spontaneous abortion; tumour; ss.

XX Synthetic.

XX WO200014217-A2.
XX 16-MAR-2000.
XX
PF 03-SEP-1999; 99WO-BP06502.
XX
PR 03-SEP-1998; 98EP-0116652.
XX
PA (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.
XX
PI Wagner H, Lipford GB, Heeg K;
XX
XX WPI; 2000-256970/22.
XX
Compositions comprising G-motif oligonucleotides useful for treating
PT e.g. septic shock, rheumatoid arthritis, diabetes and human
PT immunodeficiency virus infections -
XX
XX Example 14; Page 32; 75pp; English.

XX The present sequence represents a G-motif oligonucleotide of the
CC invention. The specification describes compositions comprising G-motif
CC oligonucleotides. The G-motif oligonucleotides inhibit activation of
CC antigen presenting cells by inhibiting the uptake of DNA by a cell, by
CC stimulating natural killer cells, or by co-stimulating cytotoxic
CC T-lymphocytes. The G-motif oligonucleotides may be used for the
CC productions of vaccines for treating septic shock, inflammation,
CC autoimmune diseases (e.g. rheumatoid arthritis, Crohn's disease,
CC sarcoidosis, multiple sclerosis, Kawasaki syndrome, graft-versus-host

CC disease and transplant rejection), helper T cell response 1-mediated
CC diseases (e.g. Streptococcal induced arthritis, Lyme arthritis, chronic
CC inflammatory bowel disease, psoriasis vulgaris, experimental allergic
CC encephalomyelitis, and insulin-dependent diabetes mellitus), bacterial
CC infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis),
CC viral infections (e.g. Cytomegalovirus and human immunodeficiency virus
CC (HIV)-infections), spontaneous abortions and tumours. They may also be
CC used to induce proliferation of bone marrow cells, especially macrophage
CC precursor cells.

XX Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;

Query Match 85.7%; Score 18; DB 21; Length 18;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGGAGGGGGTGGTGGGG 21
|||
Db 1 TTGGAGGGGGTGGTGGGG 18

RESULT 8
AAZ99650/c
ID AAZ99650 standard; DNA; 18 BP.
XX
AC AAZ99650;
XX
DT 12-JUL-2000 (first entry)
XX
DE Nucleotide sequence of non-G-motif oligonucleotide GRF1comp.

XX G-motif oligonucleotide; vaccine; Toxoplasmosis; viral infection;
KW antigen presenting cell activation; natural killer cell; septic shock;
KW cytotoxic T-lymphocyte; inflammation; autoimmune disease;
KW rheumatoid arthritis; Crohn's disease; sarcoidosis; multiple sclerosis;
KW Kawasaki syndrome; graft-versus-host disease; transplant rejection;
KW helper T cell response 1-mediated disease; Lyme arthritis;
KW Streptococcal induced arthritis; chronic inflammatory bowel disease;
KW psoriasis vulgaris; experimental allergic encephalomyelitis;
KW insulin-dependent diabetes mellitus; bacterial infection;
KW parasitic infection; Leishmaniasis; spontaneous abortion; tumour; ss.

XX Synthetic.

XX WO200014217-A2.
XX 16-MAR-2000.
XX
PF 03-SEP-1999; 99WO-BP06502.
XX
PR 03-SEP-1998; 98EP-0116652.
XX
PA (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.
XX
PI Wagner H, Lipford GB, Heeg K;
XX
XX WPI; 2000-256970/22.
XX
Compositions comprising G-motif oligonucleotides useful for treating
PT e.g. septic shock, rheumatoid arthritis, diabetes and human
PT immunodeficiency virus infections -
XX
XX Example 14; Page 32; 75pp; English.

XX The present sequence represents a non-G-motif oligonucleotide of the
CC invention. The specification describes compositions comprising G-motif
CC oligonucleotides. The G-motif oligonucleotides inhibit activation of
CC antigen presenting cells by inhibiting the uptake of DNA by a cell, by
CC stimulating natural killer cells, or by co-stimulating cytotoxic
CC T-lymphocytes. The G-motif oligonucleotides may be used for the
CC productions of vaccines for treating septic shock, inflammation,
CC autoimmune diseases (e.g. rheumatoid arthritis, Crohn's disease,
CC sarcoidosis, multiple sclerosis, Kawasaki syndrome, graft-versus-host

CC disease and transplant rejection), helper T cell response 1-mediated
 CC diseases (e.g. Streptococcal induced arthritis, Lyme arthritis, chronic
 CC inflammatory bowel disease, psoriasis vulgaris, experimental allergic
 CC encephalomyelitis, and insulin-dependent diabetes mellitus), bacterial
 CC infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis),
 CC viral infections (e.g. Cytomegalovirus and human immunodeficiency virus
 CC (HIV)-infections), spontaneous abortions and tumours. they may also be
 CC used to induce proliferation of bone marrow cells, especially macrophage
 CC precursor cells.

XX Sequence 18 BP; 4 A; 13 C; 0 G; 1 T; 0 other;
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Query Match 85.7%; Score 18; DB 21; Length 18;

Best Local Similarity 100.0%; Pred. No. 7e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TTGGAGGGGGTGGTGGGG 21

DB 18 TTGGAGGGGGTGGTGGGG 1

RESULT 9

AAT36243

ID AAT36243 standard; DNA; 18 BP.

XX AC AAT36243;

XX DT 25-MAR-2003 (updated)

XX DT 16-APR-1997 (first entry)

XX DE CD28 expression inhibiting oligonucleotide, RT09s.

XX KW Reduction; T cell; CD28; gene expression; treatment; immune system;
 KW disorder; graft versus host disease; septic shock; viral disease;
 KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;
 KW multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2;
 KW systemic lupus erythematosus; inflammatory bowel disease;
 KW IL-2; production; antisense; inhibition; ss

XX OS Synthetic.
 XX PN WO9624380-A1.
 XX PD 15-AUG-1996.

XX PF 05-FEB-1996; 96WO-US01507.

XX PR 09-FEB-1995; 95US-0387041.
 XX PR 18-SEP-1995; 95US-0529878.

XX PR 09-FEB-1995; 95US-0387041.
 XX PR 18-SEP-1995; 95US-0529878.

XX PA (ICNC) ICN PHARM INC.

XX PI Tam RC;

XX XX WPI; 1996-384228/38.

XX Oligo:nucleotide which reduces CD28 gene expression in T cells -
 PT for treating immune system diseases, e.g. graft vs. host disease,
 PT septic shock, psoriasis, etc.
 XX Example 2; Page 45; 77pp; English.

XX The present oligonucleotide reduces CD28 dependent interleukin-2
 CC (IL-2) production and T cell CD28 gene expression, useful in the
 CC treatment of CD28 mediated diseases, particularly immune system
 CC disorders, e.g. graft versus host disease, septic shock, viral
 CC disease, psoriasis, type I diabetes mellitus, thyroiditis,
 CC sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis,
 CC systemic lupus erythematosus, inflammatory bowel disease, etc..
 CC Reducing CD28 expression may reduce the effects of antigenic
 CC stimulation of CD28 positive T cells, with a consequent reduction

CC in cytokine release.
 CC (Updated on 25-MAR-2003 to correct PR field.)

XX SQ Sequence 18 BP; 2 A; 0 C; 13 G; 3 T; 0 other;
 SQ

Query Match 78.1%; Score 16.4; DB 17; Length 18;

Best Local Similarity 94.4%; Pred. No. 2.7e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 TTGGAGGGGGTGGTGGGG 21

DB 1 TTGGAGGGGGGAGGTGGGG 18

RESULT 10

AAX90336

ID AAX90336 standard; DNA; 18 BP.

XX AC AAX90336;

XX DT 24-SEP-1999 (first entry)

XX DE CD28 inhibiting phosphorothioate oligonucleotide RT09S.

XX KW CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
 KW immune system mediated disease; gamma-interferon; IL-8;
 KW phosphorothioate; ss.

XX OS Synthetic.

XX PN US5932556-A.

XX PD 03-AUG-1999.

XX PF 18-SEP-1995; 95US-0529878.

XX PR 18-SEP-1995; 95US-0529878.

XX PA (TAMR/) TAM R C.

XX PI Tam RC;

XX XX WPI; 1999-443609/37.

XX Treatment of immune system-mediated diseases by inhibiting
 PT expression of CD28, IL-2, gamma-interferon or IL-8

XX PS Example; Column 24; 45pp; English.

XX CC The present invention describes a method for inhibiting the expression
 CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
 CC comprises subcutaneous administration of an oligonucleotide (OGN).
 CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
 CC method. The OGNs are used for the treatment of immune system-mediated
 CC diseases. The present sequence represents a CD28 inhibiting
 CC phosphorothioate oligonucleotide used in the exemplification of the
 CC present invention.

XX SQ Sequence 18 BP; 2 A; 0 C; 13 G; 3 T; 0 other;
 SQ

Query Match 78.1%; Score 16.4; DB 20; Length 18;

Best Local Similarity 94.4%; Pred. No. 2.7e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 TTGGAGGGGGTGGTGGGG 21

DB 1 TTGGAGGGGGGAGGTGGGG 18

RESULT 11

AAT36242

ID AAT36242 standard; DNA; 18 BP.

XX

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AC AAT36242;
XX
DT 25-MAR-2003 (updated)
DT 16-APR-1997 (first entry)
XX
DE CD28 expression inhibiting oligonucleotide, RT05s.
XX
DE Reduction; T cell; CD28; gene expression; treatment; immune system;
KW disorder; graft versus host disease; septic shock; viral disease;
KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;
KW multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2;
KW systemic lupus erythematosus; inflammatory bowel disease;
KW IL-2; production; antisense; inhibition; ss
XX
OS Synthetic.
XX
PN WO9624380-A1.
XX
PD 15-AUG-1996.
XX
PF 05-FEB-1996; 96WO-US01507.
XX
PR 09-FEB-1995; 95US-0387041.
XX
PR 18-SEP-1995; 95US-0529878.
XX
PR 09-FEB-1995; 95US-0387041.
XX
PR 18-SEP-1995; 95US-0529878.
XX
PA (ICNC ) ICN PHARM INC.
XX
PI Tam RC;
XX
DR WPI; 1996-384228/38.
XX
PT Oligo-nucleotide which reduces CD28 gene expression in T cells -
PT for treating immune system diseases, e.g. Graft vs. host disease,
PT septic shock, psoriasis, etc.
XX
XX Example 2; Page 45; 77pp; English.
XX
CC The present oligonucleotide reduces CD28 dependent interleukin-2
CC (IL-2) production and T cell CD28 gene expression, useful in the
CC treatment of CD28 mediated diseases, particularly immune system
CC disorders, e.g. graft versus host disease, septic shock, viral
CC disease, psoriasis, type I diabetes mellitus, thyroiditis,
CC sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis,
CC systemic lupus erythematosus, inflammatory bowel disease, etc.
CC Reducing CD28 expression may reduce the effects of antigenic
CC stimulation of CD28 positive T cells, with a consequent reduction
CC in cytokine release.
CC (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 18 BP; 3 A; 0 C; 13 G; 2 T; 0 other;
Query Match 70.5%; Score 14.8; DB 17; Length 18;
Best Local Similarity 88.9%; Pred. No. 1e+04; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;
Qy 4 TTGGAGGGGTGGTGGG 21
Db 1 TTGGAGGGGTGGTGGG 18
RESULT 12
AAT36244
ID AAT36244 standard; DNA; 18 BP.
XX
AC AAT36244;
XX
DT 25-MAR-2003 (updated)
DT 16-APR-1997 (first entry)
XX
DE CD28 expression inhibiting oligonucleotide, RT10s.
XX

```

```

KW Reduction; T cell; CD28; gene expression; treatment; immune system;
KW disorder; graft versus host disease; septic shock; viral disease;
KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;
KW multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2;
KW systemic lupus erythematosus; inflammatory bowel disease;
KW IL-2; production; antisense; inhibition; ss
XX
OS Synthetic.
XX
PN WO9624380-A1.
XX
PD 15-AUG-1996.
XX
PF 05-FEB-1996; 96WO-US01507.
XX
PR 09-FEB-1995; 95US-0387041.
XX
PR 18-SEP-1995; 95US-0529878.
XX
PR 09-FEB-1995; 95US-0387041.
XX
PR 18-SEP-1995; 95US-0529878.
XX
PA (ICNC ) ICN PHARM INC.
XX
PI Tam RC;
XX
DR WPI; 1996-384228/38.
XX
PT Oligo-nucleotide which reduces CD28 gene expression in T cells -
PT for treating immune system diseases, e.g. Graft vs. host disease,
PT septic shock, psoriasis, etc.
XX
XX Example 2; Page 45; 77pp; English.
XX
CC The present oligonucleotide reduces CD28 dependent interleukin-2
CC (IL-2) production and T cell CD28 gene expression, useful in the
CC treatment of CD28 mediated diseases, particularly immune system
CC disorders, e.g. graft versus host disease, septic shock, viral
CC disease, psoriasis, type I diabetes mellitus, thyroiditis,
CC sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis,
CC systemic lupus erythematosus, inflammatory bowel disease, etc.
CC Reducing CD28 expression may reduce the effects of antigenic
CC stimulation of CD28 positive T cells, with a consequent reduction
CC in cytokine release.
CC (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 18 BP; 1 A; 2 C; 11 G; 4 T; 0 other;
Query Match 70.5%; Score 14.8; DB 17; Length 18;
Best Local Similarity 88.9%; Pred. No. 1e+04; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;
Qy 4 TTGGAGGGGTGGTGGG 21
Db 1 TTGGAGGGGTGGTGGG 18
RESULT 13
AAX90335
ID AAX90335 standard; DNA; 18 BP.
XX
AC AAX90335;
XX
DT 24-SEP-1999 (first entry)
XX
DE CD28 inhibiting phosphorothioate oligonucleotide RT05S.
XX
DE CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
KW immune system mediated disease; gamma-interferon; IL-8;
KW phosphorothioate; ss.
XX
OS Synthetic.
XX
PN US9932556-A.
XX

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PD 03-AUG-1999.
XX
XX PF 18-SEP-1995; 95US-0529878.
XX
XX PR 18-SEP-1995; 95US-0529878.
XX
XX (TAMR/) TAM R C.
XX
XX PA Tam RC;
XX
XX PI WPI; 1999-443609/37.
XX
XX DR Treatment of immune system-mediated diseases by inhibiting
XX PT expression of CD28, IL-2, gamma-interferon or IL-8
XX
XX PS Example; Column 24; 45pp; English.
XX
XX CC The present invention describes a method for inhibiting the expression
XX CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
XX CC comprises subcutaneous administration of an oligonucleotide (OGN).
XX CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
XX CC method. The OGNs are used for the treatment of immune system-mediated
XX CC diseases. The present sequence represents a CD28 inhibiting
XX CC phosphorothioate oligonucleotide used in the exemplification of the
XX CC present invention.
XX
XX SQ Sequence 18 BP; 3 A; 0 C; 13 G; 2 T; 0 other;

Query Match 70.5%; Score 14.8; DB 20; Length 18;
Best Local Similarity 88.9%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TTGGAGGGGGTGGTGGG 21
DB 1 TTGGAGGGGGAGGAGGGG 18

RESULT 14
AAX90337
ID AAX90337 standard; DNA; 18 BP.
XX
XX AC AAX90337;
XX
XX DT 24-SEP-1999 (first entry)
XX
XX DE CD28 inhibiting phosphorothioate oligonucleotide RT10S.
XX
XX KW CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
XX KW immune system mediated disease; gamma-interferon; IL-8;
XX KW phosphorothioate; ss.
XX
XX OS Synthetic.
XX
XX PI US5932556-A.
XX
XX PN 03-AUG-1999.
XX
XX PD 18-SEP-1995; 95US-0529878.
XX
XX PF 18-SEP-1995; 95US-0529878.
XX
XX PR 18-SEP-1995; 95US-0529878.
XX
XX PA (TAMR/) TAM R C.
XX
XX PI Tam RC;
XX
XX DR WPI; 1999-443609/37.
XX
XX CC Treatment of immune system-mediated diseases by inhibiting
XX PT expression of CD28, IL-2, gamma-interferon or IL-8
XX
XX PS Example; Column 24; 45pp; English.
XX
XX CC The present invention describes a method for inhibiting the expression

of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
comprises subcutaneous administration of an oligonucleotide (OGN).
AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
method. The OGNs are used for the treatment of immune system-mediated
diseases. The present sequence represents a CD28 inhibiting
phosphorothioate oligonucleotide used in the exemplification of the
present invention.

Sequence 18 BP; 1 A; 2 C; 11 G; 4 T; 0 other;

Query Match 70.5%; Score 14.8; DB 20; Length 18;
Best Local Similarity 88.9%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TTGGAGGGGGTGGTGGG 21
DB 1 TTGGAGGGGGTGGTGGG 18

RESULT 15
AAQ81074
ID AAQ81074 standard; DNA; 20 BP.
XX
XX AC AAQ81074;
XX
XX DT 25-MAR-2003 (updated)
XX
XX DT 22-SEP-1995 (first entry)
XX
XX DE supF gene triplex forming mutagenic oligonucleotide pso-AGT20.
XX
XX KW supF gene; triplex forming mutagenic oligonucleotide; pso-AGT20;
XX KW 4'hydroxymethyl-4,5',8-trimethylpsoralenated; site specific; ss.
XX
XX OS Synthetic.
XX
XX FH Key
XX FT modified_base 1
XX FT /*tag= a
XX FT /note= "4'hydroxymethyl-4,5',
XX FT 8-trimethylpsoralenated"
XX
XX PN WO9501364-A1.
XX
XX PD 12-JAN-1995.
XX
XX PF 24-JUN-1994; 94WO-US07234.
XX
XX PR 25-JUN-1993; 93US-0083088.
XX
XX PA (UYVA ) UNIV YALE.
XX
XX PI Glazer PM, Havre PA;
XX
XX XX WPI; 1995-060943/08.
XX
XX DR New mutagenic oligo:nucleotide(s) - having a mutagen incorporated
XX PT in an oligo:nucleotide which forms a triplex, for site-directed
XX PT mutagenesis
XX
XX PS Example 5; Page 38; 72pp; English.
XX
XX CC AAQ81074 is the supF gene triplex forming mutagenic oligonucleotide
XX CC pso-AGT20. It forms a triplex (a triple stranded nucleic acid) with
XX CC a specific site on the supF genome, enabling the covalently bound
XX CC 4'hydroxymethyl-4,5',8-trimethylpsoralen group to produce a site
XX CC specific mutation.
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX SQ Sequence 20 BP; 3 A; 0 C; 15 G; 2 T; 0 other;

Query Match 67.6%; Score 14.2; DB 16; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.7e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 2 GGAAGGGGGGGTGGTGG 20
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Search completed: October 27, 2003, 11:25:19
Job time : 189 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:29 ; Search time 1845.4 Seconds
(without alignments)
276.576 Million cell updates/sec

Title: US-09-331-204A-6
Perfect score: 21
Sequence: 1 999ttggagg999tgc9999 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 11152

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST.*

1: em_estba:*
2: em_esthum:*
3: em_estin:*
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6: em_estpi:*
7: em_estro:*
8: em_estc:*
9: gb_est1:*
10: gb_est2:*
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13: gb_est5:*
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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	14.6	69.5	22	28	AZ645874
C 2	14.6	69.5	22	28	AZ766712
C 3	14.6	69.5	22	28	AZ871408
C 4	13.6	64.8	20	28	AZ666896

C 5	13.6	64.8	20	28	AZ959440
C 6	13.6	64.8	21	28	AZ476392
C 7	13.6	64.8	22	9	AA911600
C 8	13.6	64.8	22	13	BQ585098
C 9	13.6	64.8	22	28	AZ331988
C 10	13.6	64.8	22	28	AZ607348
C 11	13.6	64.8	22	28	AZ868780
C 12	13.2	62.9	21	28	AZ468862
C 13	13	61.9	21	13	BQ590339
C 14	13	61.9	21	13	BQ591392
C 15	13	61.9	21	13	BQ591421
C 16	13	61.9	21	28	AZ307440
C 17	13	61.9	21	28	AZ309910
C 18	13	61.9	21	28	AZ326151
C 19	13	61.9	21	28	AZ345376
C 20	13	61.9	21	28	AZ345432
C 21	13	61.9	21	28	AZ349570
C 22	13	61.9	21	28	AZ374427
C 23	13	61.9	21	28	AZ375567
C 24	13	61.9	21	28	AZ379925
C 25	13	61.9	21	28	AZ404075
C 26	13	61.9	21	28	AZ433710
C 27	13	61.9	21	28	AZ441558
C 28	13	61.9	21	28	AZ479786
C 29	13	61.9	21	28	AZ486754
C 30	13	61.9	21	28	AZ486758
C 31	13	61.9	21	28	AZ627987
C 32	13	61.9	21	28	AZ629261
C 33	13	61.9	21	28	AZ648382
C 34	13	61.9	21	28	AZ654886
C 35	13	61.9	21	28	AZ655958
C 36	13	61.9	21	28	AZ665155
C 37	13	61.9	21	28	AZ762085
C 38	13	61.9	21	28	AZ764510
C 39	13	61.9	21	28	AZ764596
C 40	13	61.9	21	28	AZ769435
C 41	13	61.9	21	28	AZ775790
C 42	13	61.9	21	28	AZ779114
C 43	13	61.9	21	28	AZ782599
C 44	13	61.9	21	28	AZ783943
C 45	13	61.9	21	28	AZ784621

ALIGNMENTS

RESULT 1
AZ645874/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

AZ645874 22 bp DNA linear GSS 14-DEC-2000
IM0511C07R Mouse 10kb plasmid UUGClM library Mus musculus genomic
clone UUGClM0511C07 R, genomic survey sequence.
AZ645874
AZ645874.1 GI:11775791
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
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 Seq primer: CACACAGGAAACAGCTATGACC
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 High quality sequence stop: 22.
 Location/Qualifiers

FEATURES

source

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/db_xref="taxon:10090"
/clone="UUGCLM0511C07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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BASE COUNT 0 a 21 c 0 g 1 t
 ORIGIN

Query Match 69.5%; Score 14.6; DB 28; Length 22;
 Best Local Similarity 81.0%; Pred. NO. 3.1e-05;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGTTGGAGGGGGTGGTGGG 21
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 Db 22 GGGGGGGAGGGGGGGGGGGG 2

RESULT 2

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 LOCUS
 DEFINITION 1M0564A03R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
 Clone UUGCLM0564A03 R, genomic survey sequence.

ACCESSION AZ766712.1 GI:12884063
 VERSION
 KEYWORDS
 SOURCE

Mus musculus (house mouse)
 Mus musculus

ORGANISM
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.

Mus whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL

Unpublished

Contact: Robert B. Weiss

University of Utah

Genome Center

University of Utah

Rm. 308, Biomedical

Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
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 Seq primer: CACACAGGAAACAGCTATGACC
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 Location/Qualifiers

FEATURES

source

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/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

BASE COUNT 1 a 21 c 0 g 0 t
 ORIGIN

Query Match 69.5%; Score 14.6; DB 28; Length 22;
 Best Local Similarity 81.0%; Pred. NO. 3.1e-05;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGTTGGAGGGGGTGGTGGG 21
 |||||
 Db 21 GGGGTGGGGGGGGGGGGGGG 1

RESULT 3

AZ871408/c 22 bp DNA linear GSS 21-FEB-2001
 LOCUS
 DEFINITION 2M0184E16F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
 Clone UUGCLM0184E16 F, genomic survey sequence.

ACCESSION AZ871408
 VERSION
 KEYWORDS
 SOURCE

Mus musculus (house mouse)
 Mus musculus

ORGANISM
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.

Mus whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL

Unpublished

Contact: Robert B. Weiss

University of Utah

Genome Center

University of Utah

Rm. 308, Biomedical

Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: cdunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0184 row: E column: 16

Seq primer: CGTTGTAACAGCGGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

FEATURES

source

1..22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0184E16"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

BASE COUNT 0 a 21 c 0 g 1 t

ORIGIN

Query Match 59.5%; Score 14.6; DB 28; Length 22;

Best Local Similarity 81.0%; Pred. No. 3.1e+05;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGTGGAGGGGGGTGGTGGGG 21

DB 21 GGGGGGAGGGGGGGGGGGGGG 1

RESULT 4

AZ666896/c

LOCUS

IM0549A24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0549A24 F, genomic survey sequence.

ACCESSION

AZ666896

VERSION

AZ666896.1 GI:11804042

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 20)

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished

CONTACT: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

94112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: cdunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0549 row: A column: 24

Seq primer: CTTGTAACAGCGGCCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1..20

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0549A24"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

BASE COUNT 1 a 19 c 0 g 0 t

ORIGIN

Query Match 64.8%; Score 13.6; DB 28; Length 20;

Best Local Similarity 80.0%; Pred. No. 6.2e+05;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGTGGAGGGGGGTGGTGGGG 21

DB 20 GGTGGGGGGGGGGGGGGGGG 1

RESULT 5

AZ959440/c

LOCUS

2M0242032F Mouse 10kb plasmid UUGC2M library Mus musculus genomic

clone UUGC2M0242032 F, genomic survey sequence.

ACCESSION

AZ959440

VERSION

AZ959440.1 GI:13840667

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 20)

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished

CONTACT: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0242 row: 0 column: 12
 Seq primer: CGTTGTAAGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers

FEATURES

source

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M0242012"
/sex="Female"
/lab host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      0 a      19 c      0 g      1 t
ORIGIN

```

```

Query Match      64.8%; Score 13.6; DB 28; Length 20;
Best Local Similarity 80.0%; Pred.No. 6.2e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY  2  GGTTGAGGGGGTGTGGGG 21
    |||||
Db   20  GGGGGGAGGGGGGGGGGG 1

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RESULT 6
AZ476392/c      21 bp  DNA      linear      GSS 04-OCT-2000
LOCUS
DEFINITION
  1M0295F12F Mouse 10kb plasmid UUC2M library Mus musculus genomic
  clone UUC2M0295F12 F, genomic survey sequence.
ACCESSION
  AZ476392
VERSION
  AZ476392.1 GI:10634517
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 21)
REFERENCE
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
  ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
  and Wright,D.,Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
JOURNAL
  Unpublished
COMMENT
  Contact: Robert B. Weiss
  University of Utah Genome Center

```

University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0295 row: F column: 12
 Seq primer: CGTTGTAAGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers

FEATURES

source

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1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0295F12"
/sex="Male"
/lab host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      0 a      20 c      0 g      1 t
ORIGIN

```

```

Query Match      64.8%; Score 13.6; DB 28; Length 21;
Best Local Similarity 80.0%; Pred.No. 6.2e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY  1  GGTTGAGGGGGTGTGGG 20
    |||||
Db   20  GGGGGGAGGGGGGGGGGG 1

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RESULT 7
AA911600      22 bp  mRNA      linear      EST 21-APR-1998
LOCUS
DEFINITION
  0490D06.s1 NCI_CGAP Bx5 Homo sapiens cDNA clone IMAGE:1377515
  similar to TR:Q18444 Q1844 COSMID C34D4. ;contains PTRS.t3 TAR1
  repetitive element ;, mRNA sequence.
ACCESSION
  AA911600
VERSION
  AA911600.1 GI:3050964
SOURCE
  EST.
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 22)
REFERENCE
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
JOURNAL
  Unpublished
COMMENT
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
  Tissue Procurement: Ilan Kirsch, M.D., Kristina A. Cole, M.D.,

```

Ph.D. student, Rodrigo P. Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: David B. Krizman, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Insert Length: 255 Std Error: 0.00
 Seq primer: -40m13 fwd. BT from Amersham
 High quality sequence stop: 1.

FEATURES

Location/Qualifiers
 1..22
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:137515"
 /sex="female"
 /tissue_type="infiltrating ductal carcinoma"
 /lab_host="DH10B"
 /clone_lib="NCI-CGAP Br5"
 /note="Organ: breast; Vector: pAMP10; mRNA made from infiltrating ductal carcinoma, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp." 3 t

BASE COUNT

1 a 1 c 17 g 3 t

Query Match

Best Local Similarity 64.8%; Score 13.6; DB 9; Length 22;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGTTGGAGGGGGTGGGG 20

Db 3 GGGTGGCGGGGGTGGGG 22

RESULT 8

B0585098

LOCUS

DEFINITION B0585098 22 bp mRNA linear EST 06-DEC-2002

CDNA clone 024-002-K08-SP6 MP12-ADIS-024-inflorescence Beta vulgaris

ACCESSION B0585098

VERSION

KEYWORDS

SOURCE

ORGANISM

Beta vulgaris

Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 22)

Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,

Drungowski,M., Stahl,D., Wuck,M., Menze,A., O'Brien,J., Lehrach,H.

and Radloff,U.

Construction of a 'unigene' cDNA clone set by oligonucleotide

fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

Contact: Weisshaar B

ADIS DNA core facility at MP12

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@mp12-koeln.mpg.de

Insert Length: 22 Std Error: 0.00

Plate: 2 row: K column: 08

Seq primer: SP6; CATACGATTAGGTGACACTATAG.

Location/Qualifiers

1..22

/organism="Beta vulgaris"

/mol_type="mRNA"

/cultivar="KWS2320 (double haploid, monogerm breeding line

)"

/db_xref="GABI:181599"

/db_xref="taxon:161934"

/clone="024-002-K08"

/tissue_type="inflorescence"

/lab_host="EMDH10B"

/clone_lib="MP12-ADIS-024-inflorescence"

/note="Vector: pCMVSP08T6; Site 1: SalI; Site 2: NotI;

cDNA library from sugar beet, library provided by KWS

Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:

b.schulz@kws.de; cloning sites SalI-NotI, primer sites and

orientation:

SP6-SalI-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:

sequencing granted in the context of the GABI-beet project

local PI: Dr. Katharina Schneider, coordinator: Prof.

Christian Jung; Sequence submission managed by

RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

BASE COUNT 0 a 0 c 21 g 0 t 1 others

Query Match

Best Local Similarity 64.8%; Score 13.6; DB 13; Length 22;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGGTTGGAGGGGGTGGGG 21

Db 1 GCGGGGNGGGGGGGGGGG 21

RESULT 9

AZ331988

LOCUS

DEFINITION

1M0060B11F Mouse 10kb plasmid UUGCLM library Mus musculus genomic

clone UUGCLM0060B11 F, genomic survey sequence.

ACCESSION AZ331988

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 22)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.

and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Place: 0060 row: B column: 11

Seq primer: CCGTGAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1..22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGCLM0060B11"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGCLM library"

/note="Vector: PWB42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 1 a 0 c 21 g 0 t

ORIGIN

Query Match 64.8%; Score 13.6; DB 28; Length 22;
 Best Local Similarity 80.0%; Pred. No. 6.2e+05;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGTTGGAGGGGGTGGTGGG 20
 |||||
 Db 3 GGGGGGAGGGGGGGGGGGG 22

RESULT 10
 AZ607348/c
 LOCUS
 DEFINITION
 1M0429P18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0429P18 R, genomic survey sequence.

ACCESSION
 AZ607348
 VERSION
 GSS.
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0429 row: D column: 18
 Seq primer: CACACAGGAACACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 22.

FEATURES
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0429P18"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42mv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 21 c 0 g 1 t

ORIGIN

Query Match 64.8%; Score 13.6; DB 28; Length 22;
 Best Local Similarity 80.0%; Pred. No. 6.2e+05;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGTTGGAGGGGGTGGTGGG 20
 |||||
 Db 20 GGGGGGAGGGGGGGGGGGG 1

RESULT 11
 AZB68780
 LOCUS
 DEFINITION
 2M0180E12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0180E12 R, genomic survey sequence.

ACCESSION
 AZB68780
 VERSION
 GSS.
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0180 row: E column: 12
 Seq primer: CACACAGGAACACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 22.

FEATURES
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 1. .22
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
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 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 1 a 0 c 17 g 4 t
 ORIGIN
 Query Match 64.8%; Score 13.6; DB 28; Length 22;
 Best Local Similarity 80.0%; Pred. No. 6.2e+05;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGTTGGAGGGGGTGGTGGG 20
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RESULT 12
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 LOCUS
 DEFINITION
 clone UUGC1M0282004 F, genomic survey sequence.

ACCESSION
 AZ468862
 VERSION
 GSS.
 KEYWORDS
 Mus musculus (house mouse)
 SOURCE
 ORGANSIM

REFERENCE
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 21)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.
 and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

UNPUBLISHED
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: rdunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0282 row: 0 column: 04
 Seq primer: GGTGTAAACGACGCCAGT
 Class: plasmid ends

High quality sequence stop: 21.

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 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 0 a 1 c 15 g 5 t
 ORIGIN
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 Best Local Similarity 83.3%; Pred. No. 8.3e+05;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TTGGAGGGGGTGGTGGGG 21
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 Db 1 TTGGGGGGTGGGGTGGG 18

RESULT 13
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 LOCUS
 DEFINITION
 E012845-024-019-H11-T7 MP12-ADIS-024-storage root Beta vulgaris
 cDNA clone 024-019-H11 3-PRIME, mRNA sequence.

ACCESSION
 BQ590339
 VERSION
 EST.
 KEYWORDS
 Beta vulgaris

ORGANSIM
 Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 1 (bases 1 to 21)

REFERENCE
 AUTHORS
 Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M.,
 Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
 and Radelof, U.

Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 Plant J. 32 (5), 845-857 (2002)

CONTACT: Weishaar B

ADIS DNA core facility at MPIZ
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851
 Email: weissaha@mpiz-koeln.mpg.de

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 Plate: 19 row: H column: 11

Seq primer: T7: GTAATACGACTCATTATAGGC.
 Location/Qualifiers

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)")
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cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-Noti, primer sites and
orientation:
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-Noti-T7; Note:
Sequencing granted in the context of the GABI-Beet project
, local PI: Dr. Katharina Schneider, coordinator: Prof.
Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
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ORIGIN
Query Match      61.9%; Score 13; DB 13; Length 21;
Best Local Similarity 76.2%; Pred. No. 9.5e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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RESULT 14
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LOCUS      21 bp      mRNA      linear      EST 06-DEC-2002
DEFINITION E012713-024-017-014-T7 MP1Z-ADIS-024-storage root Beta vulgaris
ACCESSION  BQ591392
VERSION    BQ591392.1 GI:26120975
KEYWORDS   EST.
SOURCE     Beta vulgaris
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE  1 (bases 1 to 21)
AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
          fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL   Plant J. 32 (5), 845-857 (2002)
COMMENT   Contact: Weisshaar B
          ADIS DNA core facility at MP1Z
          Max-Planck-Institute for Plant Breeding Research
          Carl-von-Linne Weg 10, 50629 Koeln, Germany
          Fax: 00492215062851
          Email: weisshaar@mpi-z-koeln.mpg.de
          Insert Length: 21 Std Error: 0.00
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              cDNA library from sugar beet, library provided by KWS
              Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
              b.schulz@kws.de; cloning sites Sali-Noti, primer sites and
              orientation:
              SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-Noti-T7; Note:
              Sequencing granted in the context of the GABI-Beet project
              , local PI: Dr. Katharina Schneider, coordinator: Prof.
              Christian Jung; Sequence submission managed by
              RZPD/GABI-Primary database: http://gabi.rzpd.de"

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BASE COUNT      0 a      21 c      0 g      0 t
ORIGIN
Query Match      61.9%; Score 13; DB 13; Length 21;
Best Local Similarity 76.2%; Pred. No. 9.5e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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DEFINITION E012714-024-017-P09-T7 MP1Z-ADIS-024-storage root Beta vulgaris
ACCESSION  BQ591421
VERSION    BQ591421.1 GI:26121004
KEYWORDS   EST.
SOURCE     Beta vulgaris
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE  1 (bases 1 to 21)
AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
          fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL   Plant J. 32 (5), 845-857 (2002)
COMMENT   Contact: Weisshaar B
          ADIS DNA core facility at MP1Z
          Max-Planck-Institute for Plant Breeding Research
          Carl-von-Linne Weg 10, 50629 Koeln, Germany
          Fax: 00492215062851
          Email: weisshaar@mpi-z-koeln.mpg.de
          Insert Length: 21 Std Error: 0.00
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              /mol_type="mRNA"
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              cDNA library from sugar beet, library provided by KWS
              Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
              b.schulz@kws.de; cloning sites Sali-Noti, primer sites and
              orientation:
              SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-Noti-T7; Note:
              Sequencing granted in the context of the GABI-Beet project
              , local PI: Dr. Katharina Schneider, coordinator: Prof.
              Christian Jung; Sequence submission managed by
              RZPD/GABI-Primary database: http://gabi.rzpd.de"

```

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BASE COUNT      0 a      0 c      21 g      0 t
ORIGIN
Query Match      61.9%; Score 13; DB 13; Length 21;
Best Local Similarity 76.2%; Pred. No. 9.5e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGGTTGGAGGGGGTGGTGGGG 21
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Db 1 GGGGGGGGGGGGGGGGGGG 21

Search completed: October 27, 2003, 13:59:26
Job time : 1847.4 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:34 ; Search time 48.2 Seconds
(without alignments)
192.304 Million cell updates/sec

Title: US-09-331-204A-6

Perfect score: 21
Sequence: 1 999999999999999999 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 376294

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	21	100.0	21	2	US-08-529-878B-4
2	21	100.0	21	2	US-08-529-878B-45
3	18	85.7	18	2	US-08-529-878B-3
4	18	85.7	18	2	US-08-529-878B-44
5	14.2	67.6	20	2	US-08-476-712-2
6	14.2	67.6	20	4	US-09-411-291-2
7	13.6	64.8	20	3	US-09-262-773-204
8	13.2	62.9	20	2	US-08-890-980-56
9	13.2	62.9	20	3	US-08-890-979-56
10	13.2	62.9	20	3	US-09-032-894-56
11	13.2	62.9	20	3	US-09-031-626-56
12	13.2	62.9	20	4	US-09-422-978-9409
13	13	61.9	21	1	US-07-873-915A-3
14	13	61.9	21	1	US-08-257-964-3
15	13	61.9	21	2	US-08-863-639A-11
16	13	61.9	21	2	US-08-863-639A-12
17	13	61.9	21	2	US-08-863-639A-48
18	13	61.9	21	2	US-08-863-639A-76
19	13	61.9	22	2	US-08-403-888A-36
20	13	61.9	22	2	US-08-403-888A-44
21	13	61.9	22	2	US-08-403-888A-110
22	13	61.9	22	2	US-08-403-888A-117
23	12.8	61.0	17	4	US-09-495-140-26
24	12.8	61.0	18	3	US-09-017-974-57
25	12.8	61.0	18	4	US-08-682-255A-57
26	12.8	61.0	18	4	US-09-429-130-57
27	12.8	61.0	20	1	US-08-167-113-16

Sequence 16, Appl
Sequence 35, Appl
Sequence 7, Appl
Sequence 8, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 17, Appl
Sequence 175, App
Sequence 36, Appl
Sequence 50, Appl
Sequence 73, Appl
Sequence 88, Appl
Sequence 24, Appl
Sequence 64, Appl
Sequence 3, Appl
Sequence 4, Appl
Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-08-529-878B-4
; Sequence 4, Application US/08529878B
; Patent No. 5932556
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Crockett & Fish
; STREET: 3000 S. Augusta Court
; CITY: La Habra
; STATE: California
; COUNTRY: United States of America
; ZIP: 90631
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/529,878B
; FILING DATE: 13-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Fish, Robert D.
; REGISTRATION NUMBER: 33,880
; REFERENCE/DOCKET NUMBER: 213/003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-525-3433
; TELEFAX: 714-525-3303
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-529-878B-4

Query Match 100.0%; Score 21; DB 2; Length 21;

Best Local Similarity 100.0%; Pred. No. 4.1; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GGGTTGGAGGGGGTGGTGGG 21

RESULT 2
US-08-529-878B-45
; Sequence 45, Application US/08529878B
; Patent No. 5932556
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Crockett & Fish
; STREET: 3000 S. Augusta Court
; CITY: La Habra
; STATE: California
; COUNTRY: United States of America
; ZIP: 90631
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/529,878B
; FILING DATE: 13-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Fish, Robert D.
; REGISTRATION NUMBER: 33,880
; REFERENCE/DOCKET NUMBER: 213/003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-525-3433
; TELEFAX: 714-525-3303
; MOLECULE TYPE: DNA (genomic)
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MEDIUM TYPE: DNA (genomic)
; US-08-529-878B-45
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Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GGGTTGGAGGGGTGGTGGG 21
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; Sequence 3, Application US/08529878B
; Patent No. 5932556
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Crockett & Fish
; STREET: 3000 S. Augusta Court
; CITY: La Habra
; STATE: California
; COUNTRY: United States of America
; ZIP: 90631
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/529,878B
; FILING DATE: 13-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Fish, Robert D.
; REGISTRATION NUMBER: 33,880
; REFERENCE/DOCKET NUMBER: 213/003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-525-3433
; TELEFAX: 714-525-3303
; MOLECULE TYPE: DNA (genomic)
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MEDIUM TYPE: DNA (genomic)
; US-08-529-878B-3
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Best Local Similarity 100.0%; Pred. No. 58;
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Db 1 TTGGAGGGGGTGGTGGG 18
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; Sequence 44, Application US/08529878B
; Patent No. 5932556
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Crockett & Fish
; STREET: 3000 S. Augusta Court
; CITY: La Habra
; STATE: California
; COUNTRY: United States of America
; ZIP: 90631
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/529,878B
; FILING DATE: 13-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Fish, Robert D.
; REGISTRATION NUMBER: 33,880
; REFERENCE/DOCKET NUMBER: 213/003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-525-3433
; TELEFAX: 714-525-3303
; MOLECULE TYPE: DNA (genomic)
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MEDIUM TYPE: DNA (genomic)
; US-08-529-878B-44
Query Match 85.7%; Score 18; DB 2; Length 18;

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Best Local Similarity 100.0%; Pred. No. 58;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGGAGGGGGTGTGGGG 21
Db 1 TTGGAGGGGGTGTGGGG 18

RESULT 5
US-08-476-712-2
; Sequence 2, Application US/08476712
; Patent No. 5962426
; GENERAL INFORMATION:
; APPLICANT: Glaxo, Peter, M.
; TITLE OF INVENTION: Triple-Helix Forming Oligonucleotides for
; TITLE OF INVENTION: Targeted Mutagenesis
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,712
; FILING DATE: 7-JUNE-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: YU114
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-873-8794
; TELEFAX: (404)-873-8795
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-476-712-2

Query Match 67.6%; Score 14.2; DB 2; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGTGGAGGGGTGTGGG 20
Db 2 GGAAGGGGGGTGTGGG 20

RESULT 6
US-09-411-291-2
; Sequence 2, Application US/09411291
; Patent No. 6303376
; GENERAL INFORMATION:
; APPLICANT: Glaxo, Peter, M.
; TITLE OF INVENTION: Triple-Helix Forming Oligonucleotides for
; TITLE OF INVENTION: Targeted Mutagenesis
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/411,291
; FILING DATE: 04-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,712
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: YU114
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-873-8794
; TELEFAX: (404)-873-8795
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-411-291-2

Query Match 67.6%; Score 14.2; DB 4; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGTGGAGGGGTGTGGG 20
Db 2 GGAAGGGGGGTGTGGG 20

RESULT 7
US-09-262-773-204
; Sequence 204, Application US/09262773
; Patent No. 6225451
; GENERAL INFORMATION:
; APPLICANT: Ballinger, Dennis G.
; APPLICANT: Ding, Wei
; APPLICANT: Wagner, Susanne
; APPLICANT: Hees, Mark A.
; TITLE OF INVENTION: CHROMOSOME 11-LINKED CORONARY HEART DISEASE
; TITLE OF INVENTION: SUSCEPTIBILITY GENE CHD1
; FILE REFERENCE: Myriad 3
; CURRENT APPLICATION NUMBER: US/09/262,773
; CURRENT FILING DATE: 1999-03-04
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 204
; LENGTH: 20
; TYPE: DNA
; ORGANISM: DNA fragment
US-09-262-773-204

Query Match 64.8%; Score 13.6; DB 3; Length 20;
Best Local Similarity 80.0%; Pred. No. 2.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGTGGAGGGGTGTGGG 20
Db 1 GGTGGGGGGGTGTGGGG 20

RESULT 8
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US-08-890-980-56/c
; Sequence 56, Application US/08890980
; Patent No. 598141
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: SR-B1 NUCLEIC ACIDS AND USES THEREFOR
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,980
; FILING DATE: 10-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MIA-005.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer"
US-08-890-980-56
Query Match 62.9%; Score 13.2; DB 2; Length 20;
Best Local Similarity 83.3%; Pred. No. 4e+03; 3; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 GTTGGAGGGGGTGGTGGG 20
Db 20 GTGGGCTGGGGTGGTGGG 3
RESULT 9
US-08-890-979-56/c
; Sequence 56, Application US/08890979
; Patent No. 6030778
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Ordovas, Jose M.
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS
; TITLE OF INVENTION: DISORDERS
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,979

; FILING DATE: 10-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MIA-005.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer"
US-08-890-979-56
Query Match 62.9%; Score 13.2; DB 3; Length 20;
Best Local Similarity 83.3%; Pred. No. 4e+03; 3; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 GTTGGAGGGGGTGGTGGG 20
Db 20 GTGGGCTGGGGTGGTGGG 3
RESULT 10
US-09-032-894-56/c
; Sequence 56, Application US/09032894
; Patent No. 6130041
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: SR-B1 NUCLEIC ACIDS AND USES THEREFOR
; FILE REFERENCE: MIA-005.03
; CURRENT APPLICATION NUMBER: US/09/032,894
; CURRENT FILING DATE: 1998-02-27
; EARLIER APPLICATION NUMBER: 08/890,980
; EARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-032-894-56
Query Match 62.9%; Score 13.2; DB 3; Length 20;
Best Local Similarity 83.3%; Pred. No. 4e+03; 3; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 GTTGGAGGGGGTGGTGGG 20
Db 20 GTGGGCTGGGGTGGTGGG 3
RESULT 11
US-09-031-626-56/c
; Sequence 56, Application US/09031626
; Patent No. 6228581
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Ordovas, Jose M.
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MIA-005.04
; CURRENT APPLICATION NUMBER: US/09/031,626
; CURRENT FILING DATE: 1998-02-27
; EARLIER APPLICATION NUMBER: 08/890,979
; EARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 56
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
; US-09-031-626-56

Query Match      62.9%; Score 13.2; DB 3; Length 20;
Best Local Similarity 83.3%; Pred. No. 4e+03;
Matches 15; Conservative 0; Mismatches 0; Gaps 0;

QY 3 GTTGGAGGGGTGGTGGG 20
Db 20 GTGGGCTGGGGTGGTGGG 3

RESULT 12
US-09-422-978-9409/C
; Sequence 9409, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilyia
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020Cp1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 9409
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: downstream amplification primer 99-449 for SEQ 1544, in complement
; US-09-422-978-9409

Query Match      62.9%; Score 13.2; DB 4; Length 20;
Best Local Similarity 83.3%; Pred. No. 4e+03;
Matches 15; Conservative 0; Mismatches 0; Gaps 0;

QY 1 GGTTGGAGGGGTGGTG 18
Db 20 GAGTTGGAGGGGAGATG 3

RESULT 13
US-07-873-915A-3
; Sequence 3, Application US/07873915A
; Patent No. 5348868
; GENERAL INFORMATION:
; APPLICANT: Reddy, Parameswara M.
; APPLICANT: Hanna, Naam B.
; TITLE OF INVENTION: Methods and Reagents
; TITLE OF INVENTION: for Cleaving and
; TITLE OF INVENTION: Protecting
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Beckman Instruments, Inc.
; STREET: 2500 Harbor Boulevard
; CITY: Fullerton
; STATE: California
; COUNTRY: USA
; ZIP: 92634
; COMPUTER READABLE FORM:

; SEQ ID NO 9409
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: downstream amplification primer 99-449 for SEQ 1544, in complement
; US-09-422-978-9409
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; MEDIUM TYPE: Diskette, 3.5 inch,
; MEDIUM TYPE: 1.44 Mb
; COMPUTER: IBM
; OPERATING SYSTEM: MS.DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/873,915A
; FILING DATE: 19920424
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Burgoon, Richard P.
; REGISTRATION NUMBER: 34,787
; REFERENCE/DOCKET NUMBER: 128D-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 773-7610
; TELEFAX: (714) 773-7936
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 bases
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: no
; ANTI-SENSE: no
; US-07-873-915A-3

Query Match      61.9%; Score 13; DB 1; Length 21;
Best Local Similarity 76.2%; Pred. No. 4.8e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGTTGGAGGGGTGGTGGG 21
Db 1 GGGGGGGGGGGGGGGGGGG 21

RESULT 14
US-08-257-964-3
; Sequence 3, Application US/08257964
; Patent No. 5518651
; GENERAL INFORMATION:
; APPLICANT: Reddy, Parameswara M.
; APPLICANT: Hanna, Naam B.
; TITLE OF INVENTION: Methods and Reagents
; TITLE OF INVENTION: for Cleaving and
; TITLE OF INVENTION: Protecting
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Beckman Instruments, Inc.
; STREET: 2500 Harbor Boulevard
; CITY: Fullerton
; STATE: California
; COUNTRY: USA
; ZIP: 92634
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch,
; MEDIUM TYPE: 1.44 Mb
; COMPUTER: IBM
; OPERATING SYSTEM: MS.DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/257,964
; FILING DATE: June 8, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C.
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 128D-1175A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 773-6971
; TELEFAX: (714) 773-7936
; INFORMATION FOR SEQ ID NO: 3:
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SEQUENCE CHARACTERISTICS:

LENGTH: 21 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: no
ANTI-SENSE: no
US-08-257-964-3

Query Match 61.9%; Score 13; DB 1; Length 21;
Best Local Similarity 76.2%; Pred. No. 4.8e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGTTGAGGGGGTGGTGGGG 21
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Db 1 GGGGGGGGGGGGGGGGGGGG 21

RESULT 15

US-08-863-639A-11/c
Sequence 11, Application US/08863639A
Patent No. 5981185

GENERAL INFORMATION:

APPLICANT: Matson, Robert S.
APPLICANT: Coassin, Peter J.
APPLICANT: Rampal, Jang B.
APPLICANT: Caskey, C. T.
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:

ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, 9th Floor
CITY: Pasadena
STATE: CA
COUNTRY: USA
ZIP: 91101

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage

COMPUTER: IBM compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: Corel WordPerfect 8 version

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/863,639A

FILING DATE: May 28, 1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Joseph E. Mueth

REGISTRATION NUMBER: 20,532

REFERENCE/DOCKET NUMBER: 11859-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (626) 796-4000

TELEFAX: (626) 795-6321

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Other nucleic acid

US-08-863-639A-11

Query Match 61.9%; Score 13; DB 2; Length 21;
Best Local Similarity 76.2%; Pred. No. 4.8e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 21 GGGGGGGGGGGGGGGGGGGG 1

Search completed: October 27, 2003, 14:03:34
Job time : 48.2 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 11:25:34 ; Search time 452.6 Seconds

(without alignments)
124.432 Million cell updates/sec

Title: US-09-331-204A-6

Perfect score: 21

Sequence: 1 99gttgagggtgtgtggg 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1792395 seqs, 134090451 residues

Total number of hits satisfying chosen parameters: 408622

Minimum DB seq length: 0

Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA.*

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3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCRUS_PUBCOMB.seq.*
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9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
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14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	13.4	63.8	20	10	US-09-874-162A-22
C 2	13.2	62.9	20	11	US-09-779-152-56
C 3	13.2	62.9	20	14	US-10-023-610-56
C 4	13	61.9	17	11	US-09-740-332-2132
C 5	13	61.9	17	11	US-09-740-332-2133
C 6	13	61.9	17	11	US-09-740-332-2422
C 7	13	61.9	17	11	US-09-740-332-2423
C 8	13	61.9	17	12	US-09-817-879-2132
C 9	13	61.9	17	12	US-09-817-879-2133
C 10	13	61.9	17	12	US-09-817-879-2422
C 11	13	61.9	17	12	US-09-817-879-2423
C 12	13	61.9	21	9	US-09-828-034-31
C 13	12.8	61.0	17	12	US-10-059-877-26
C 14	12.8	61.0	17	12	US-10-303-108A-30
C 15	12.8	61.0	17	14	US-10-059-888-26
C 16	12.8	61.0	18	12	US-10-204-884-59

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17 12.8 61.0 20 14 US-10-181-846-35 Sequence 35, Appl
c 18 12.8 61.0 22 11 US-09-888-115A-3 Sequence 3, Appl
c 19 12.8 61.0 22 11 US-09-888-115A-13 Sequence 13, Appl
c 20 12.8 61.0 22 11 US-09-888-115A-20 Sequence 20, Appl
c 21 12.8 61.0 22 11 US-09-888-115A-22 Sequence 22, Appl
c 22 12.6 60.0 20 9 US-09-854-883-175 Sequence 175, Appl
c 23 12.6 60.0 21 9 US-09-828-034-11 Sequence 11, Appl
c 24 12.6 60.0 21 9 US-09-828-034-30 Sequence 30, Appl
c 25 12.6 60.0 21 11 US-09-832-300-24 Sequence 24, Appl
c 26 12.6 60.0 21 12 US-10-083-246A-78 Sequence 78, Appl
c 27 12.6 60.0 21 12 US-10-184-085A-227 Sequence 227, Appl
c 28 12.4 59.0 20 12 US-10-032-585-5333 Sequence 5333, Ap
c 29 12.2 58.1 17 10 US-09-363-959-904 Sequence 904, App
c 30 12.2 58.1 17 11 US-09-818-875-295 Sequence 295, App
c 31 12.2 58.1 17 11 US-09-818-875-296 Sequence 296, App
c 32 12.2 58.1 18 10 US-09-369-373-1900 Sequence 1900, Ap
c 33 12.2 58.1 18 10 US-09-263-959-921 Sequence 921, App
c 34 12.2 58.1 18 14 US-10-196-460-4 Sequence 4, Appl
c 35 12.2 58.1 19 12 US-10-318-628-9 Sequence 9, Appl
c 36 12.2 58.1 20 9 US-09-854-883-174 Sequence 174, App
c 37 12.2 58.1 20 10 US-09-755-004-10 Sequence 10, Appl
c 38 12.2 58.1 20 12 US-09-767-421-36 Sequence 36, Appl
c 39 12.2 58.1 20 12 US-10-279-579A-47 Sequence 47, Appl
c 40 12.2 58.1 22 11 US-09-918-896-23 Sequence 23, Appl
c 41 12.2 58.1 22 11 US-09-918-896-24 Sequence 24, Appl
c 42 12.2 58.1 22 11 US-09-905-588C-14 Sequence 14, Appl
c 43 12 57.1 20 10 US-09-800-266A-133 Sequence 133, App
c 44 12 57.1 20 10 US-09-895-007A-133 Sequence 133, App
c 45 12 57.1 20 10 US-09-920-313-133 Sequence 133, App
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ALIGNMENTS

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RESULT 1
US-09-874-162A-22/c
; Sequence 22, Application US/09874162A
; Patent No. US2002015542A1
; GENERAL INFORMATION:
; APPLICANT: Koontz, Jason
; APPLICANT: Sklar, Jeffrey
; TITLE OF INVENTION: FUSION OF JAZF1 AND UJAZ1 GENES IN
; TITLE OF INVENTION: ENDOMETRIAL STROMAL TUMORS
; FILE REFERENCE: 05311-024001
; CURRENT APPLICATION NUMBER: US/09/874,162A
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 60/209,093
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for PCR
US-09-874-162A-22
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Query Match 63.8%; Score 13.4; DB 10; Length 20;
Best Local Similarity 93.3%; Pred. No. 2.3e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 6 GGAGGGGGTGTGGG 20

Db 19 GGAGGGGGTGTGGG 5

RESULT 2

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US-09-779-152-56/c
; Sequence 56, Application US/09779152
; Publication No. US2003004782A1
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
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Query Match 61.9%; Score 13; DB 11; Length 17;
Best Local Similarity 84.6%; Pred. No. 3.3e+04;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGGGGTGGTGGG 21
| | | | | | | | | | | | | | | | |
Db 5 GGGGGUGUGGGG 17

RESULT 7

US-09-740-332-2423
; Sequence 2423, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2423
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-2423

Query Match 61.9%; Score 13; DB 11; Length 17;
Best Local Similarity 84.6%; Pred. No. 3.3e+04;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGGGGTGGTGGG 21
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Db 2 GGGGGUGUGGGG 14

RESULT 8

US-09-817-879-2132/c
; Sequence 2132, Application US/09817879
; Publication No. US2003017131A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MBH00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2132
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-2132

Query Match 61.9%; Score 13; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGGGGTGGTGGG 21
| | | | | | | | | | | | | | | | |
Db 17 GGGGGTGGTGGG 5

RESULT 9

US-09-817-879-2133/c
; Sequence 2133, Application US/09817879
; Publication No. US2003017131A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MBH00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2133
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-2133

Query Match 61.9%; Score 13; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGGGGTGGTGGG 21
| | | | | | | | | | | | | | | | |
Db 14 GGGGGTGGTGGG 2

RESULT 10

US-09-817-879-2422
; Sequence 2422, Application US/09817879
; Publication No. US2003017131A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MBH00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2422
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-2422

Query Match 61.9%; Score 13; DB 12; Length 17;
Best Local Similarity 84.6%; Pred. No. 3.3e+04;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGGGGTGGTGGG 21
| | | | | | | | | | | | | | | | |
Db 5 GGGGGUGUGGGG 17

RESULT 11

US-09-817-879-2423
; Sequence 2423, Application US/09817879
; Publication No. US2003017131A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MBH00-801-F

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; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2423
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-2423

```

Query Match 61.9%; Score 13; DB 12; Length 17;
Best Local Similarity 84.6%; Pred. No. 3.3e+04;
Matches 11; Conservative 2; Mismatches 0; Indels

Qy 9 GGGGGTGGTGGG 21
| | | | | : | | |
Db 2 GGGGGUGGUGGG 14

RESULT 12

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US-09-828-034-31/C
; Sequence 31, Application US/09828034
; Patent No. US20020064771A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Weidong
; APPLICANT: Hong, Zhi
; APPLICANT: Ferrari, Eric
; TITLE OF INVENTION: HCV REPLICASE COMPOSITIONS
; FILE REFERENCE: IN011465
; CURRENT APPLICATION NUMBER: US/09/828034
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: U.S. 60/160000
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 31
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Feature 31
US-09-828-034-31

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Query Match 61.9%; Score 13; DB 9; Length 21;
Best Local Similarity 76.2%; Pred. NO. 3.2e+04;
Matches 16; Conservative 0; Mismatches 5; Indels

Qy 1 GGGTTGGAGGGGGTGGTGGG 21
| | | | | | | | | |
Db 21 GTGGTGGTGGTGGTGGTG 1

RESULT 13

```

US-10-059-877-26
; Sequence 26, Application US/10059877
; Publication No. US20030157490A1
; GENERAL INFORMATION:
; APPLICANT: CHAO, LEE
; APPLICANT: CHAO, JULIE
; APPLICANT: SONG, QING
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TISSUE KALLIKREIN INHIBITION
; TITLE OF INVENTION: TISSUE KALLIKREIN INHIBITION
; TITLE OF INVENTION: HYPERTENSION
; FILE REFERENCE: 1913.008192
; CURRENT APPLICATION NUMBER: US/10/059877
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: 09/495,141
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 09/389,561

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; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 08/856,141
; PRIOR FILING DATE: 1997-05-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: synthetic construct
US-10-059-877-26

```

Query Match	61.0%;	Score 12.8;	DB 12;	Length 17;
Best Local Similarity	87.5%;	Pred. No. 4e+04;		
Matches 14;	Conservative	0;	Mismatches 2;	Indels

Qy 6 GGAGGGGGTGGTGGG 21
Db 1 GGAGGGGGGGGGGGG 16

RESULT 14

```

RESOLI 14
US-10-303-109A-30/c
; Sequence 30, Application US/10303109A
; Publication No. US20030194726A1
; GENERAL INFORMATION:
; APPLICANT: BOLCHAKOVA, Elena
; APPLICANT: ROZZELLE, James
; TITLE OF INVENTION: Thermus Oshimai Nucleic Acid Polymerases
; FILE REFERENCE: 4777US
; CURRENT APPLICATION NUMBER: US/10/303.109A
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/334,798
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Thermus oshimai
US-10-303-109A-30

```

```
Query Match      61.0%; Score 12.8; DB 12; Length 17;
Best Local Similarity 87.5%; Pred. No. 4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels
```

Qy 5 TGGAGGGGGTGGTGG 20
Db 16 TGGAGGTGGAGGTGG 1

RESULT 15

US-10-059-888-26
Sequence 26, Application US/10059888
Publication No. US2003025862A1
GENERAL INFORMATION:
APPLICANT: CHAO, LEE
APPLICANT: CHAO, JULIE
APPLICANT: SONG, QING
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING
TITLE OF INVENTION: TISSUE KALLIKREIN GENE PROMOTER POLYMORPHISMS WITH ESSENTIAL
TITLE OF INVENTION: HYPERINSON
FILE REFERENCE: 19113.0081U2
CURRENT APPLICATION NUMBER: US/10/059,888
CURRENT FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: 09/495,140
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 09/389,566
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 08/856,141
PRIOR FILING DATE: 1997-05-14

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; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030025882A1e =
; OTHER INFORMATION: synthetic construct
US-10-059-888-26

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Query Match      61.0%; Score 12.8; DB 14; Length 17;
Best Local Similarity 87.5%; Pred. No. 4e+04; 2; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 2;

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Qy      6 GGAGGGGGTGGTGGGG 21
        |||||
Db      1 GGAGGGGGGGGGGG 16

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Job time : 453.6 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:35 ; Search time 2749 Seconds
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253.343 Million cell updates/sec

Title: US-09-331-204A-6

Perfect score: 21

Sequence: 1 ggggtgaggggggtggggggg 21

Scoring table: IDENTITY NUC

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Searched: 33363688 seqs, 1658189874 residues

Total number of hits satisfying chosen parameters: 2938060

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	ID	Description
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2	21	19	US-09-331-204A-6
3	21	19	US-09-331-204A-6
4	18	8	US-08-387-041A-3

; TYPE: DNA
; ORGANISM: synthetic construct
US-09-331-204A-6

Query Match 100.0%; Score 21; DB 19; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTTGAGGGGTGTGGG 21
| | | | | | | | | | | | | | | | | | | | | |
Db 1 GGGTTGAGGGGTGTGGG 21

RESULT 4

US-08-387-041A-3
; Sequence 3, Application US/08387041A
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATION
; TITLE OF INVENTION: OF CD28 EXPRESSION
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/387,041A
; FILING DATE: 02-FEB-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8250-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-387-041A-3

Query Match 85.7%; Score 18; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTGGAGGGGTGTGGG 21
| | | | | | | | | | | | | | | | | | | | | |
Db 1 TTGGAGGGGTGTGGG 18

RESULT 5

US-09-331-204-1
; Sequence 1, Application US/09331204
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert
; TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN
; TITLE OF INVENTION: IMMUNE RESPONSE
; FILE REFERENCE: ICNSequence
; CURRENT APPLICATION NUMBER: US/09/331,204
; CURRENT FILING DATE: 1999-08-20

; PRIOR APPLICATION NUMBER: PCT/US97/23927
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: An oligomer
; OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic
; OTHER INFORMATION: acid including oligomers consisting of naturally
; OTHER INFORMATION: occurring bases, sugars and intersugar
US-09-331-204-1

Query Match 85.7%; Score 18; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTGGAGGGGTGTGGG 21
| | | | | | | | | | | | | | | | | | | | | |
Db 1 TTGGAGGGGTGTGGG 18

RESULT 6

US-09-331-204A-4
; Sequence 4, Application US/09331204A
; GENERAL INFORMATION:
; APPLICANT: ICN Pharmaceuticals, Inc.
; APPLICANT: Tam, Robert
; TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Resp
; FILE REFERENCE: 216/013-US1
; CURRENT APPLICATION NUMBER: US/09/331,204A
; CURRENT FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US97/23927
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 18
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-331-204A-4

Query Match 85.7%; Score 18; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTGGAGGGGTGTGGG 21
| | | | | | | | | | | | | | | | | | | | | |
Db 1 TTGGAGGGGTGTGGG 18

RESULT 7

US-09-786-436-17
; Sequence 17, Application US/09786436
; GENERAL INFORMATION:
; APPLICANT: Wagner, Hermann
; APPLICANT: Lipford, Grayson
; APPLICANT: Heeg, Klaus
; TITLE OF INVENTION: G-Motif Oligonucleotides and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: C1041/7010 (AWS)
; CURRENT APPLICATION NUMBER: US/09/786,436
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: PCT/EP99/06502
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
US-09-786-436-17

Query Match 85.7%; Score 18; DB 33; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGGAGGGGGTGGTGGGG 21
|||||
Db 1 TTGGAGGGGGTGGTGGGG 18

RESULT 8

US-09-786-436-42/c
Sequence 42, Application US/09786436
GENERAL INFORMATION:
APPLICANT: Wagner, Hermann
APPLICANT: Lipford, Grayson
APPLICANT: Heeg, Klaus
TITLE OF INVENTION: G-Motif Oligonucleotides and Uses
TITLE OF INVENTION: Thereof
FILE REFERENCE: C1041/7010 (AWS)
CURRENT APPLICATION NUMBER: US/09/786.436
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: PCT/EP99/06502
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 42
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
US-09-786-436-42

Query Match 85.7%; Score 18; DB 33; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGGAGGGGGTGGTGGGG 21
|||||
Db 18 TTGGAGGGGGTGGTGGGG 1

RESULT 9

US-09-331-204-5
Sequence 5, Application US/09331204
GENERAL INFORMATION:
APPLICANT: Tam, Robert
TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN
TITLE OF INVENTION: IMMUNE RESPONSE
FILE REFERENCE: ICNSequence
CURRENT APPLICATION NUMBER: US/09/331,204
CURRENT FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: PCT/US97/23927
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: An oligomer
OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic
OTHER INFORMATION: acid. This term includes oligomers consisting of
OTHER INFORMATION: naturally occurring bases, sugars and intersugar (

Query Match 78.1%; Score 16.4; DB 19; Length 18;
Best Local Similarity 94.4%; Pred. No. 4.5e-04;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 TTGGAGGGGGTGGTGGGG 21
|||||
Db 1 TTGGAGGGGGAGGTGGGG 18

RESULT 10

US-09-331-204A-8
Sequence 8, Application US/09331204A
GENERAL INFORMATION:
APPLICANT: ICN Pharmaceuticals, Inc.
APPLICANT: Tam, Robert
TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Res
FILE REFERENCE: 216/013-US1
CURRENT APPLICATION NUMBER: US/09/331,204A
CURRENT FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: PCT/US97/23927
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8
LENGTH: 18
TYPE: DNA
ORGANISM: synthetic construct
US-09-331-204A-8

Query Match 78.1%; Score 16.4; DB 19; Length 18;
Best Local Similarity 94.4%; Pred. No. 4.5e-04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TTGGAGGGGGTGGTGGGG 21
|||||
Db 1 TTGGAGGGGGAGGTGGGG 18

RESULT 11

US-09-331-204A-7
Sequence 7, Application US/09331204A
GENERAL INFORMATION:
APPLICANT: ICN Pharmaceuticals, Inc.
APPLICANT: Tam, Robert
TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Res
FILE REFERENCE: 216/013-US1
CURRENT APPLICATION NUMBER: US/09/331,204A
CURRENT FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: PCT/US97/23927
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.0
SEQ ID NO 7
LENGTH: 18
TYPE: DNA
ORGANISM: synthetic construct
US-09-331-204A-7

Query Match 70.5%; Score 14.8; DB 19; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.7e-05;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TTGGAGGGGGTGGTGGGG 21
|||||
Db 1 TTGGAGGGGGAGGTGGGG 18

RESULT 12

US-09-331-204A-9
Sequence 9, Application US/09331204A
GENERAL INFORMATION:
APPLICANT: ICN Pharmaceuticals, Inc.
APPLICANT: Tam, Robert
TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Res
FILE REFERENCE: 216/013-US1

; CURRENT APPLICATION NUMBER: US/09/331,204A
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US97/23927
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 18
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-331-204A-9

Query Match 70.5%; Score 14.8; DB 19; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.7e+05;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TTGAGGGGGTGTGGGG 21
Db 1 TTGAGGGGGTGTGGCG 18

RESULT 13

US-09-331-204-4
; Sequence 4, Application US/09331,204
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert
; TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN
; FILE REFERENCE: ICNsequence
; CURRENT APPLICATION NUMBER: US/09/331,204
; CURRENT FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US97/23927
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence. An oligomer
; OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic
; OTHER INFORMATION: acid. This term includes oligomers consisting of
; OTHER INFORMATION: naturally occurring bases, sugars and intersugar (

Query Match 70.5%; Score 14.8; DB 19; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.7e+05;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TTGAGGGGGTGTGGGG 21
Db 1 TTGAGGGGGAGGAGGGG 18

RESULT 14

US-10-303-778-3043
; Sequence 3043, Application US/10303778
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICAALLY DETECTABLE GROUP OF NOVEL VIRAL
; TITLE OF INVENTION: REGULATORY GENES AND USES THEREOF
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/10/303,778
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 17608
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3043
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-778-3043

Query Match 70.5%; Score 14.8; DB 50; Length 22;
Best Local Similarity 88.9%; Pred. No. 1.6e+05;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGTTGGAGGGGTGGTG 18
Db 5 GGGCTTGAGGGGTGGTG 22

RESULT 15

US-10-310-188-41819
; Sequence 41819, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICAALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41819
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-41819

Query Match 69.5%; Score 14.6; DB 50; Length 21;
Best Local Similarity 81.0%; Pred. No. 1.9e+05;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGTTGGAGGGGTGGTGGG 21
Db 1 GGGGAGGAGGGGTGGGCGG 21

Search completed: October 27, 2003, 17:52:53
Job time : 2750 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 11:09:34 ; Search time 358.2 Seconds
(without alignments)
97.777 Million cell updates/sec

Title: US-09-331-204A-6
Perfect score: 21
Sequence: 1 ggggtggaggggggtggtggg 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2231628 seqs, 833900706 residues

Total number of hits satisfying chosen parameters: 264402

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents, NA, New.*

- 1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq.*
- 2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
- 3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
- 4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
- 5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
- 6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 7: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.6	69.5	21	1	PCT-US02-38216-41819
2	14.6	69.5	22	1	PCT-US02-38216-51871
3	14.4	68.6	18	1	PCT-US02-38216-27376
4	14.4	68.6	18	1	PCT-US02-38216-41547
5	14.4	68.6	19	1	PCT-US02-38216-38943
6	14.4	68.6	19	1	PCT-US02-38216-46976
7	14.4	68.6	22	1	PCT-US02-38216-26689
8	14.4	68.6	22	1	PCT-US02-38216-42141
9	14.2	67.6	19	1	PCT-US02-38216-78687
10	14.2	67.6	20	5	US-09-978-333B-2
11	14.2	67.6	20	5	US-09-978-333C-2
12	14.2	67.6	21	1	PCT-US02-38216-51847
13	14.2	67.6	21	1	PCT-US02-38216-55389
14	14.2	67.6	22	1	PCT-US02-38216-63940
15	14	66.7	19	1	PCT-US02-38216-27360
16	13.8	65.7	19	1	PCT-US02-38216-18378
17	13.8	65.7	19	1	PCT-US02-38216-47426
18	13.8	65.7	19	1	PCT-US02-38216-61865
19	13.8	65.7	20	1	PCT-US02-38216-18418
20	13.8	65.7	20	1	PCT-US02-38216-39237
21	13.8	65.7	21	1	PCT-US02-38216-75562
22	13.6	64.8	21	1	PCT-US02-38216-41967
23	13.6	64.8	21	1	PCT-US02-38216-72839
24	13.6	64.8	21	1	PCT-US02-38216-78761
25	13.6	64.8	21	1	PCT-US02-38216-84959
26	13.6	64.8	22	1	PCT-US02-38216-18413

27	13.6	64.8	22	1	PCT-US02-38216-39492	Sequence 39492, A
28	13.6	64.8	22	1	PCT-US02-38216-57248	Sequence 57248, A
29	13.4	63.8	18	1	PCT-US02-38216-10539	Sequence 10539, A
30	13.4	63.8	18	1	PCT-US02-38216-38927	Sequence 38927, A
31	13.4	63.8	19	1	PCT-US02-38216-53577	Sequence 53577, A
32	13.4	63.8	20	1	PCT-US02-38216-41804	Sequence 41804, A
33	13.4	63.8	21	1	PCT-US02-38216-55622	Sequence 55622, A
34	13.4	63.8	21	1	PCT-US02-38216-57364	Sequence 57364, A
35	13.4	63.8	22	1	PCT-US02-38216-10603	Sequence 10603, A
36	13.2	62.9	18	1	PCT-US02-38216-9731	Sequence 9731, Ap
37	13.2	62.9	18	1	PCT-US02-38216-29535	Sequence 29535, A
38	13.2	62.9	18	1	PCT-US02-38216-51842	Sequence 51842, A
39	13.2	62.9	18	1	PCT-US02-38216-51896	Sequence 51896, A
40	13.2	62.9	18	1	PCT-US02-38216-61077	Sequence 61077, A
41	13.2	62.9	18	1	PCT-US02-38216-86378	Sequence 86378, A
42	13.2	62.9	19	1	PCT-US02-38216-68852	Sequence 68852, A
43	13.2	62.9	19	1	PCT-US02-38216-69453	Sequence 69453, A
44	13.2	62.9	20	1	PCT-US02-38216-10564	Sequence 10564, A
45	13.2	62.9	21	1	PCT-US02-38216-26725	Sequence 26725, A

ALIGNMENTS

RESULT 1
PCT-US02-38216-41819
; Sequence 41819, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41819
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-41819

Query Match 69.5%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 1.5e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGTTCGAGGGGTCGTCGGG 21
DB 1 GGGGAGGAGGGGTCGTCGGG 21

RESULT 2
PCT-US02-38216-51871
; Sequence 51871, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51871
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-51871

Query Match 69.5%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 1.5e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGTGGAGGGGGTGGTGGG 21
Db 1 GGGTGGGGGTGGGGGTGGG 21

RESULT 3

PCT-US02-38216-27376
; Sequence 27376, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27376
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-27376

Query Match 68.6%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.8e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GTTGGAGGGGGTGGTG 18
Db 1 GGTGGAGGGGGTGGTG 16

RESULT 4

PCT-US02-38216-41647
; Sequence 41647, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41647
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-41647

Query Match 68.6%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.8e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGAGGGGGTGGTGGG 21
Db 1 GGAGGGGGTGGAGGG 16

RESULT 5

PCT-US02-38216-38943
; Sequence 38943, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38943
; LENGTH: 19

; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-38943

Query Match 68.6%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.8e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GGAGGGGGTGGTGGG 21
Db 4 GGAGGGGGTGGCGGG 19

RESULT 6

PCT-US02-38216-46976
; Sequence 46976, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46976
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-46976

Query Match 68.6%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.8e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GGAGGGGGTGGTGGG 21
Db 4 GGTGGGGGTGGTGGG 19

RESULT 7

PCT-US02-38216-26689/c
; Sequence 26689, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26689
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-26689

Query Match 68.6%; Score 14.4; DB 1; Length 22;
Best Local Similarity 93.8%; Pred. No. 1.8e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TTGGAGGGGGTGGTG 19
Db 16 TTGGAGGGGGTGGTG 1

RESULT 8

PCT-US02-38216-42141
; Sequence 42141, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY

Query Match	67.6%;	Score 14.2;	DB 5;	Length 20;
Best Local Similarity	84.2%;	Pred. No. 2.1e+04;		

RESULT 13
PCT-US02-38216-55389/c
; Sequence 55389, Application PC/RUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DERIVED
; TITLE OF INVENTION: GENES AND USES THEREOF

Search completed: October 27, 2003, 18:22:55
Job time : 358.2 secs

FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PatentIn version 3.2
SEQ ID NO 55389
LENGTH: 21
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US02-38216-55389

Query Match 67.6%; Score 14.2; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 2.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTTGGAGGGGGTGGTGG 19
||| ||||| |||||
DB 20 GGAAGAGAGCGGTGGTGG 2

RESULT 14
PCT-US02-38216-63940
Sequence 63940, Application PC/TUS0238216
GENERAL INFORMATION:
APPLICANT: Rosetta Genomics LTD
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PatentIn version 3.2
SEQ ID NO 63940
LENGTH: 22
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US02-38216-63940

Query Match 67.6%; Score 14.2; DB 1; Length 22;
Best Local Similarity 84.2%; Pred. No. 2.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GTTGGAGGGGGTGGTGGG 21
||| ||||| ||||| |||||
DB 1 GGTGGGGGGGTGGGGGGG 19

RESULT 15
PCT-US02-38216-27360
Sequence 27360, Application PC/TUS0238216
GENERAL INFORMATION:
APPLICANT: Rosetta Genomics LTD
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
FILE REFERENCE: 55002
CURRENT APPLICATION NUMBER: PCT/US02/38216
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PatentIn version 3.2
SEQ ID NO 27360
LENGTH: 19
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US02-38216-27360

Query Match 66.7%; Score 14; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.5e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGAGGGGGTGGTGG 19
||| ||||| ||||| |||||
DB 5 GGAGGGGGTGGTGG 18

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:29 ; Search time 376.114 Seconds
(without alignments)
1957.844 Million cell updates/sec

Title: US-09-331-204A-7
Perfect score: 18
Sequence: 1 ttggaggggagagagggg 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 681044

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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2: gb_htg.*
3: gb_in.*
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33: em_htg_mus.*
34: em_htg_pln.*
35: em_htg_rod.*
36: em_htg_mam.*
37: em_htg_vrt.*
38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	15.4	85.6	21	6	A31974	A31974 Synthetic H
2	15.4	85.6	21	6	AR131393	AR131393 Sequence
3	15.4	85.6	21	6	BD001798	BD001798 Immunogen
C 4	15	83.3	17	6	AX532425	AX532425 Sequence
C 5	15	83.3	17	6	AX532426	AX532426 Sequence
C 6	15	83.3	17	6	AX532427	AX532427 Sequence
7	14.8	82.2	18	6	AX023402	AX023402 Sequence
C 8	14.8	82.2	18	6	AX023427	AX023427 Sequence
C 9	14.4	80.0	17	6	AR029938	AR029938 Sequence
C 10	14	77.8	17	6	AX532424	AX532424 Sequence
C 11	14	77.8	17	6	AX532428	AX532428 Sequence
C 12	13.8	76.7	20	6	AR232303	AR232303 Sequence
C 13	13	72.2	17	6	AX214604	AX214604 Sequence
C 14	13	72.2	17	6	AX214605	AX214605 Sequence
C 15	13	72.2	17	6	AX215457	AX215457 Sequence
C 16	13	72.2	17	6	AX215458	AX215458 Sequence
C 17	13	72.2	17	6	AX215459	AX215459 Sequence
C 18	13	72.2	17	6	AX532423	AX532423 Sequence
C 19	13	72.2	17	6	AX532429	AX532429 Sequence
C 20	12.8	71.1	17	6	AX214603	AX214603 Sequence
C 21	12.8	71.1	17	6	AX215452	AX215452 Sequence
C 22	12.8	71.1	20	6	AR126724	AR126724 Sequence
C 23	12.8	71.1	20	6	AX033457	AX033457 Sequence
C 24	12.8	71.1	20	6	AX037370	AX037370 Sequence
C 25	12.8	71.1	20	6	AX037374	AX037374 Sequence
C 26	12.8	71.1	20	6	AX241159	AX241159 Sequence
C 27	12.8	71.1	20	6	AX486754	AX486754 Sequence
C 28	12.8	71.1	21	6	AR072479	AR072479 Sequence
C 29	12.8	71.1	21	6	AR084552	AR084552 Sequence
C 30	12.8	71.1	21	6	AR084564	AR084564 Sequence
C 31	12.8	71.1	21	6	AR084570	AR084570 Sequence
C 32	12.8	71.1	21	6	AR084575	AR084575 Sequence
C 33	12.8	71.1	21	6	AR084581	AR084581 Sequence
C 34	12.8	71.1	21	6	AR084594	AR084594 Sequence
C 35	12.8	71.1	21	6	AR097224	AR097224 Sequence
C 36	12.4	68.9	15	6	A12051	A12051 Oligonucleo
C 37	12.4	68.9	15	6	A12052	A12052 Oligonucleo
C 38	12.4	68.9	17	6	AX729881	AX729881 Sequence
C 39	12.4	68.9	17	6	AX739210	AX739210 Sequence
C 40	12.4	68.9	18	6	I07756	I07756 Sequence 12
C 41	12.4	68.9	21	6	AX154328	AX154328 Sequence
C 42	12.4	68.9	21	6	AX298242	AX298242 Sequence
C 43	12.4	68.9	22	6	AR116659	AR116659 Sequence
C 44	12.4	68.9	22	6	AR233018	AR233018 Sequence
C 45	12.4	68.9	22	6	AR237949	AR237949 Sequence

ALIGNMENTS

RESULT 1

A31974

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

A31974 Synthetic HIV-1/2 diagnosis primer.
A31974
A31974.1 GI:1567257
synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 21)
Montcany M. and Montagnier, L.
Nucleotide sequences of retroviral genomes of types HIV-1, HIV-2
and HIV, their uses for the amplification of these genomes and
diagnosis in vitro of these viral infections

JOURNAL Patent: EP 0403333-A 29 19-DEC-1990;
INSTITUT PASTEUR; INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE
MEDICALE (INSERM)

FEATURES
source Location/Qualifiers

1..21
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

BASE COUNT 5 a 2 c 13 g 1 t
ORIGIN

Query Match 85.6%; Score 15.4; DB 6; Length 21;

Best Local Similarity 94.1%; Pred. No. 2.7e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGGAGGGGAGGAGGGG 18

Db 3 TGGAGGGGAGGAGGGAG 19

RESULT 2

AR131393 LOCUS 21 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 45 from patent US 6194142.
ACCESSION AR131393
VERSION AR131393.1 GI:14120296

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 21)

AUTHORS Moncany,M. and Montagnier,L.

TITLE Nucleotide sequences derived from the genome of retroviruses of the HIV-1, HIV-2, and SIV type, and their uses in particular for the

amplification of the genomes of these retroviruses and for the in vitro diagnosis of the diseases due to these viruses

Patent: US 6194142-A 45 27-FEB-2001;

Location/Qualifiers

1..21

/organism="unknown"

BASE COUNT 5 a 2 c 13 g 1 t

ORIGIN

Query Match

Best Local Similarity 85.6%; Score 15.4; DB 6; Length 21;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGGAGGGGAGGAGGGG 18

Db 3 TGGAGGGGAGGAGGGAG 19

RESULT 3

BD001798 LOCUS 21 bp DNA linear PAT 31-JAN-2002
DEFINITION Immunogenic compounds containing a translation product of nucleotide sequence from retrovirus genome of HIV-1, HIV-2 and SIV types.

ACCESSION BD001798

VERSION BD001798.1 GI:18626357

KEYWORDS JP 2000093187-A/45.

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 21)

AUTHORS Moncany,M. and Montagnier,L.

TITLE Immunogenic compounds containing a translation product of nucleotide sequence from retrovirus genome of HIV-1, HIV-2 and SIV types

Patent: JP 2000093187-A 45 04-APR-2000;

INST PASTEUR,INST NATL DE LA SANTE & DE LA RECHERCHE MEDICAL

OS Artificial sequence

PN JP 2000093187-A/45

PD 04-APR-2000

PF 24-SEP-1999 JP 1999270165

PR 02-JUN-1989 FR 89/07354,20-SEP-1989 FR 89/12371 PI

MAURICE MONCANY,LUC MONTAGNIER

PC C12N15/09,A61K39/21,A61K48/00,A61P31/18,C07H21/04,C07K14/155,

C07K14/16,

PC C12Q1/68,C12Q1/70,G01N33/569,C12N15/00

CC

PH Key Location/Qualifiers

PT source 1..21

FT Location/Qualifiers

1..21 /organism="Artificial Sequence".

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

BASE COUNT 5 a 2 c 13 g 1 t

ORIGIN

Query Match 85.6%; Score 15.4; DB 6; Length 21;

Best Local Similarity 94.1%; Pred. No. 2.7e+04;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGGAGGGGAGGAGGGG 18

Db 3 TGGAGGGGAGGAGGGAG 19

RESULT 4

AX532425/c

LOCUS 17 bp DNA linear PAT 22-NOV-2002

DEFINITION Sequence 1934 from Patent EP1239051.

ACCESSION AX532425

VERSION AX532425.1 GI:25256625

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Shannon,M.

TITLE Human posh-like protein 1

JOURNAL Patent: EP 1239051-A 1934 11-SEP-2002;

Neomica, Inc. (US)

FEATURES

source 1..17

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

BASE COUNT 1 a 12 c 0 g 4 t

ORIGIN

Query Match 83.3%; Score 15; DB 6; Length 17;

Best Local Similarity 100.0%; Pred. No. 4.2e+04;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGGGGAGGAGGGG 18

Db 17 GAGGGGGAGGAGGGG 3

RESULT 5

AX532426/c

LOCUS 17 bp DNA linear PAT 22-NOV-2002

DEFINITION Sequence 1935 from Patent EP1239051.

ACCESSION AX532426

VERSION AX532426.1 GI:25256627

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

AUTHORS      Shannon,M.
TITLE        Human posh-like protein 1
JOURNAL      Patent: EP 1239051-A 1935 11-SEP-2002;
              Aeomica, Inc. (US)
FEATURES     source
              1..17
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              /mol_type="genomic DNA"
              /db_xref="taxon:9606"
BASE COUNT   1 a 12 c 0 g 4 t
ORIGIN
Query Match      83.3%; Score 15; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 GAGGGGGAGGAGGGG 18
      |||||
Db      16 GAGGGGGAGGAGGGG 2

RESULT 6
AX023427/c
LOCUS      AX023427
DEFINITION Sequence 1936 from Patent EP1239051.
ACCESSION  AX023427
VERSION     AX023427.1 GI:25256629
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Shannon,M.
TITLE       Human posh-like protein 1
JOURNAL     Patent: EP 1239051-A 1936 11-SEP-2002;
              Aeomica, Inc. (US)
FEATURES     source
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              /organism="Homo sapiens"
              /mol_type="genomic DNA"
              /db_xref="taxon:9606"
BASE COUNT   1 a 12 c 1 g 3 t
ORIGIN
Query Match      83.3%; Score 15; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 GAGGGGGAGGAGGGG 18
      |||||
Db      15 GAGGGGGAGGAGGGG 1

RESULT 7
AX023402
LOCUS      AX023402
DEFINITION Sequence 17 from Patent WO0014217.
ACCESSION  AX023402
VERSION     AX023402.1 GI:10183802
KEYWORDS    synthetic construct
              synthetic construct
              artificial sequences.
SOURCE      Lipford,G.B., Heeg,K. and Wagner,H.
ORGANISM    G-motif oligonucleotides and uses thereof
              Patent: WO 0014217-A 17 16-MAR-2000;
              LIPFORD GRAYSON B (DE) ; HEEG KLAUS (DE) ;
              WAGNER HERMANN (DE) ;
              CPG IMMUNOPHARMACEUTICALS GMBH (DE)
              Location/Qualifiers
              1..18
              /organism="synthetic construct"
FEATURES     source
              1..18
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              /mol_type="genomic DNA"
              /db_xref="taxon:9606"
BASE COUNT   1 a 12 c 1 g 3 t
ORIGIN
Query Match      83.3%; Score 15; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 GAGGGGGAGGAGGGG 18
      |||||
Db      15 GAGGGGGAGGAGGGG 1

RESULT 8
AX023427/c
LOCUS      AX023427
DEFINITION Sequence 42 from Patent WO0014217.
ACCESSION  AX023427
VERSION     AX023427.1 GI:10183827
KEYWORDS    synthetic construct
              synthetic construct
              artificial sequences.
SOURCE      Lipford,G.B., Heeg,K. and Wagner,H.
ORGANISM    G-motif oligonucleotides and uses thereof
              Patent: WO 0014217-A 42 16-MAR-2000;
              LIPFORD GRAYSON B (DE) ; HEEG KLAUS (DE) ;
              WAGNER HERMANN (DE) ;
              CPG IMMUNOPHARMACEUTICALS GMBH (DE)
              Location/Qualifiers
              1..18
              /organism="synthetic construct"
              /mol_type="genomic DNA"
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BASE COUNT   4 a 13 c 0 g 1 t
ORIGIN
Query Match      82.2%; Score 14.8; DB 6; Length 18;
Best Local Similarity 88.9%; Pred. No. 5e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TTGGAGGGGGAGGAGGGG 18
      |||||
Db      1 TTGGAGGGGGTGGTGGGG 18

RESULT 9
AR029938/c
LOCUS      AR029938
DEFINITION Sequence 127 from patent US 5861244.
ACCESSION  AR029938
VERSION     AR029938.1 GI:5943152
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Wang,C.-G. and Hepburn,A.G.
TITLE       Genetic sequence assay using DNA triple strand formation
JOURNAL     Patent: US 5861244-A 127 19-JAN-1999;
              Location/Qualifiers
              1..17
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              /mol_type="genomic DNA"
              /db_xref="taxon:32630"
BASE COUNT   0 a 12 c 0 g 5 t
ORIGIN
Query Match      80.0%; Score 14.4; DB 6; Length 17;
Best Local Similarity 93.8%; Pred. No. 7.4e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 47 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)

FEATURES
Source
1..17
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
BASE COUNT 0 a 13 c 2 g 2 t
ORIGIN

Query Match 72.2%; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred.No. 2.9e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGGGAGGAGGGG 18
|||||
Db 13 GGGGAGGAGGGG 1

RESULT 15
AX215457/c
LOCUS AX215457 17 bp mRNA linear PAT 07-SEP-2001
DEFINITION Sequence 899 from Patent WO0159103.
ACCESSION AX215457
VERSION AX215457.1 GI:15525500
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 899 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)

FEATURES
Source
1..17
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/mol_type="mRNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
BASE COUNT 0 a 14 c 0 g 3 t
ORIGIN

Query Match 72.2%; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred.No. 2.9e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGGGAGGAGGGG 18
|||||
Db 17 GGGGAGGAGGGG 5

Search completed: October 27, 2003, 11:09:26
Job time : 377.114 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:29 ; Search time 1581.77 Seconds
(without alignments)
276.576 Million cell updates/sec

Title: US-09-331-204a-8
Perfect score: 18
Sequence: 1 ttgaggggggaggtgggg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 11152

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: em_estab:*

2: em_estim:*

3: em_estim:*

4: em_estim:*

5: em_estim:*

6: em_estim:*

7: em_estim:*

8: em_estim:*

9: gb_est1:*

10: gb_est2:*

11: gb_est3:*

12: gb_est4:*

13: gb_est5:*

14: gb_est6:*

15: em_estim:*

16: em_estim:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_inv:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_nam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_fod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	13.8	76.7	19	9	AI251781
2	13.8	76.7	22	28	A2876523
C 3	13.4	74.4	22	9	AI582080
4	13.2	73.3	21	28	A2468862

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

5	12.8	71.1	19	28	A2345792	100800312
6	12.8	71.1	19	28	A2760597	1M0554M21
7	12.8	71.1	19	28	A2786308	2M0031B17
8	12.8	71.1	20	28	A2512326	1M0357118
9	12.8	71.1	20	28	A2645269	1M0510A10
10	12.8	71.1	20	28	A2659755	1M0537F22
11	12.8	71.1	20	28	A2772707	1M0583118
12	12.8	71.1	20	28	A2969440	2M0424O12
13	12.8	71.1	21	28	A2476392	1M0295F12
14	12.8	71.1	21	28	A2583408	1M0378M23
15	12.8	71.1	21	28	A2653464	1M0527G11
16	12.8	71.1	21	28	A2774703	2M0004G14
17	12.8	71.1	21	28	A2871715	2M0184B13
18	12.8	71.1	21	28	A2869578	2M0242G20
19	12.8	71.1	22	28	A2307952	1M0010J24
20	12.8	71.1	22	28	A2331988	1M0060B11
21	12.8	71.1	22	28	A2607348	1M0429D18
22	12.8	71.1	22	28	A2645874	1M0511C07
23	12.8	71.1	22	28	A2871408	2M0184E16
24	12.4	68.9	22	9	AA996014	os26408.s
25	12.4	68.9	22	28	A2797469	2M0053P10
26	12.2	67.8	18	13	BQ901245	hasp000xj
27	12.2	67.8	20	28	A2666896	1M0549A24
28	12.2	67.8	22	9	AA911600	od900d6.s
29	12.2	67.8	22	9	AI568336	tm68H08.x
30	12.2	67.8	22	28	A2766712	1M0564A03
31	11.8	65.6	19	9	AI758301	ty06407.x
32	11.8	65.6	19	28	A2783420	2M0025D07
33	11.8	65.6	21	9	AU254493	AU254493
34	11.8	65.6	21	28	A2387199	1M0146P20
35	11.8	65.6	21	28	A2394677	1M0158A24
36	11.8	65.6	21	28	A2512534	1M0358B07
37	11.8	65.6	22	9	AI434548	ti49405.x
38	11.8	65.6	22	9	AI473941	tm04c11.x
39	11.8	65.6	22	9	AI735382	at10810.x
40	11.8	65.6	22	13	BQ565098	E011826-0
41	11.8	65.6	22	28	A2447246	1M0244E23
42	11.6	64.4	19	28	A2512762	1M0358M04
43	11.6	64.4	20	28	A2845320	2M0145M02
44	11.4	63.3	16	9	AA968729	or69h11.s
45	11.4	63.3	21	28	A29555804	2M0222L03

ALIGNMENTS

RESULT 1
AI251781/c
LOCUS
DEFINITION
AI251781 19 bp mRNA linear EST 05-NOV-1998
qu76901.x1 NCI CGAP Brn35 Homo sapiens cDNA clone IMAGE:1978032.3,
similar to TR:Q39949 Q39949 HYDROXYPROLINE-RICH PROTEIN. ;, mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

AI251781.1 GI:3848310
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 19)
NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BrTAP), Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Unknown library type
Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..19

/organism="Homo sapiens"
 /mol_type="mRNA"
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 /clone="IMAGE:1978032"
 /issue_type="tumor, 5 pooled (see description)"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Brn35"
 /note="Organ: brain; Vector: PCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. 1.33 kb. Tumor types include: meningioma, oligodendroglioma, astrocytoma (grade II), medulloblastoma, astrocytoma (grade IV). Life Technologies catalog #: 11544-012"
 4 a 14 c 0 g 1 t

Query Match 76.7%; Score 13.8; DB 9; Length 19;
 Best Local Similarity 88.2%; Pred. No. 5.5e+05;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGAGGTGGG 17
 |||||

Db 17 TTGGAGGGGGAGGGGG 1

RESULT 2
 AZ876923
 LOCUS 22 bp DNA linear GSS 21-FEB-2001
 DEFINITION clone UUC2M0192D07 F, genomic survey sequence.

ACCESSION AZ876923

VERSION GSS.

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meener,E., Pedersen,T., Reilly

M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.

and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0192 row: D column: 07

Seq primer: CGTTGAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1..22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUC2M0192D07"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUC2M library"

/note="Vector: FWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 4 a 1 c 15 g 2 t

ORIGIN

Query Match 76.7%; Score 13.8; DB 28; Length 22;

Best Local Similarity 88.2%; Pred. No. 5.4e+05;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGAGGTGGG 17
 |||||

Db 2 TTGGAGGGGGAGGGGG 18

RESULT 3
 AI582080/c
 LOCUS 22 bp mRNA linear EST 06-APR-1999
 DEFINITION ar96B07.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone
 IMAGE:2173429 3' similar to SW:FOR1_MOUSE Q05859 FORMIN 4 ; contains
 element MSRI repetitive element ; mRNA sequence.

ACCESSION AI582080

VERSION AI582080.1 GI:4567977

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 22)

AUTHORS Hallier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,

Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin

J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,

White,Y., Wylie,T., Waterston,R. and Wilson,R.

WashU-NCI human EST Project

Unpublished

Contact: Willson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1..22

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2173429"

/sex="male"

/dev_stage="adult, age 25"

/lab_host="DH10B (phage resistant)"

/clone_lib="Barstead colon HPLRB7"

/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a

modified polylinker; Site 1: EcoRI; Site 2: NotI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer [5'

TGTACGATCTGAGTGGAGGGCGCCCTTTTTTTTTTTTTTT

3']; double-stranded cDNA was ligated to Eco RI adaptors

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 1 a 1 c 17 g 0 t
ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 19;
Best Local Similarity 87.5%; Pred. No. 1.1e-06;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGAGGTGGGG 18
|||
Db 2 GGGGGGAGGGGGG 17

RESULT 6

AZ760597/c 19 bp DNA linear GSS 16-FEB-2001
LOCUS
DEFINITION
1M0554N21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0554N21 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0554 row: N column: 21

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

source
1..19
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0554N21"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent *E. coli* XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 0 a 18 c 0 g 1 t
ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 19;
Best Local Similarity 87.5%; Pred. No. 1.1e+06;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGAGGTGGGG 18
|||
Db 18 GGAGGGGAGGGGGG 3

RESULT 7

AZ786308 19 bp DNA linear GSS 16-FEB-2001
LOCUS
DEFINITION
2M0031B17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0031B17 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0031 row: B column: 17

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

source
1..19
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0031B17"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 2 a 1 c 15 g 1 t
ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 19;
Best Local Similarity 87.5%; Pred. No. 1.1e+06;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGAGGGGAGGTGGGG 18
|||||

Db 1 GGGCGGGAGGTGGGG 16
|||||

RESULT 8
AZ512326/c
LOCUS 20 bp DNA linear GSS 05-OCT-2000
DEFINITION IM0357118R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0357118 R, genomic survey sequence.
ACCESSION AZ512326
VERSION AZ512326.1 GI:10693642
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0357 row: I column: 18
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0357118"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to

FEATURES
source

1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0357118"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 18 c 0 g 2 t
ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 20;
Best Local Similarity 87.5%; Pred. No. 1.1e+06;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGAGGGGAGGTGGGG 18
|||||

Db 18 GGAGGGGAGGTGGGG 3
|||||

RESULT 9
AZ45269/c
LOCUS 20 bp DNA linear GSS 14-DEC-2000
DEFINITION IM0510510R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0510510 R, genomic survey sequence.
ACCESSION AZ45269
VERSION AZ45269.1 GI:11774602
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0510 row: B column: 10
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0510510"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 19 c 0 g 1 t

ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 20;

Best Local Similarity 87.5%; Pred. No. 1.1e+06;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGAGGGGGAGGTGGGG 18

Db 17 GGAGGGGGGGGGGGG 2

RESULT 10

AZ659755/c

LOCUS

DEFINITION 1M0537F22F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0537F22 F, genomic survey sequence.

ACCESSION AZ659755

VERSION AZ659755.1

KEYWORDS GI:11796901

SOURCE GSS.

ORGANISM Mus musculus (house mouse)

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

AUTHORS 1 (bases 1 to 20)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0537 row: F column: 22

Seq primer: CGTGTAAAACGACGGCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1..20

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGCIM0537F22"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGCIM library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were

FEATURES

source

ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 18 c 0 g 2 t

ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 20;

Best Local Similarity 87.5%; Pred. No. 1.1e+06;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGAGGGGGAGGTGGGG 18

Db 20 GGAGGGGGGGGGGGG 5

RESULT 11

AZ772707/c

LOCUS

DEFINITION 1M0583L18R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0583L18 R, genomic survey sequence.

ACCESSION AZ772707

VERSION AZ772707.1

KEYWORDS GI:12896303

SOURCE GSS.

ORGANISM Mus musculus (house mouse)

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

AUTHORS 1 (bases 1 to 20)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished

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University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0583 row: L column: 18

Seq primer: CACACAGGAAACAGCATGACC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1..20

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGCIM0583L18"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGCIM library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance." 1 t

BASE COUNT
ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 20;
Best Local Similarity 87.5%; Pred. No. 1.1e+06;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGAGGTGGG 18
Db 19 GGGGGGAGGGGGG 4

RESULT 12
AZ969440/c
LOCUS 20 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0242012F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0242012 F, genomic survey sequence.

ACCESSION AZ969440
VERSION AZ969440.1 GI:13840667
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0242 row: 0 column: 12
Seq primer: CGTTGTAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1..20

FEATURES
source
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0242012"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA

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BASE COUNT
ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 20;
Best Local Similarity 87.5%; Pred. No. 1.1e+06;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGAGGTGGG 18
Db 16 GGAGGGGGGGGGGG 1

RESULT 13
AZ476392/c

LOCUS 21 bp DNA linear GSS 04-OCT-2000
DEFINITION IM0295F12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0295F12 F, genomic survey sequence.

ACCESSION AZ476392
VERSION AZ476392.1 GI:10634517
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0295 row: F column: 12
Seq primer: CGTTGTAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1..21

FEATURES
source
1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0295F12"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|9B|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN

0 a 20 c 0 g 1 t

Query Match 71.1%; Score 12.8; DB 28; Length 21;

Best Local Similarity 87.5%; Pred. No. 1.1e+06;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGAGGGGAGGTGGGG 18

Db 21 GGGGGGGAGGGGGGG 6

RESULT 14

AZ583408/c

LOCUS

DEFINITION

Clone UUGC1M0378N23 F, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112 USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0378 row: N column: 23

Seq primer: CGTTGTAAACGACGCCAGT

Class: Plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1. .21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0378N23"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|9B|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN

0 a 20 c 0 g 1 t

Query Match 71.1%; Score 12.8; DB 28; Length 21;

Best Local Similarity 87.5%; Pred. No. 1.1e+06;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGAGGGGAGGTGGGG 18

Db 18 GGAGGGGAGGGGGGG 3

RESULT 15

AZ653464/c

LOCUS

DEFINITION

Clone UUGC1M0527G11 F, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112 USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0527 row: G column: 11

Seq primer: CGTTGTAAACGACGCCAGT

Class: Plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1. .21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0527G11"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 20 c 0 g 1 t
ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 21;
Best Local Similarity 87.5%; Pred. No. 1.1e+06;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGAGGTGGG 18
|||
Db 20 GGAGGGGAGGTGGG 5

Search completed: October 27, 2003, 13:59:28
Job time : 1582.77 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:34 ; Search time 41.3143 Seconds
(without alignments)
192.304 Million cell updates/sec

Title: US-09-331-204A-8

Perfect score: 18

Sequence: 1 ttggaggagggtgggg 18

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 376294

Minimum DB seq length: 0

Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*

3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*

4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*

5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16.4	91.1	18	2	US-08-529-878B-3
2	16.4	91.1	18	2	US-08-529-878B-44
3	16.4	91.1	21	2	US-08-529-878B-4
4	16.4	91.1	21	2	US-08-529-878B-45
5	13.8	76.7	20	3	US-09-487-368A-174
6	13.8	76.7	20	4	US-09-629-644A-174
7	13.8	76.7	21	3	US-09-092-077-45
8	13.4	74.4	19	1	US-08-242-664-37
9	13.4	74.4	19	1	US-08-484-138-37
10	13.4	74.4	19	5	PCT-US95-06379-37
11	13.4	74.4	20	4	US-09-432-978-9409
12	12.8	71.1	17	2	US-08-173-489C-127
13	12.8	71.1	17	4	US-09-435-140-26
14	12.8	71.1	18	2	US-08-639-501-72
15	12.8	71.1	18	3	US-09-044-946-72
16	12.8	71.1	18	3	US-09-044-908-72
17	12.8	71.1	20	3	US-09-487-368A-175
18	12.8	71.1	20	4	US-09-056-285A-32
19	12.8	71.1	20	4	US-09-629-644A-175
20	12.8	71.1	21	2	US-08-633-575B-19
21	12.8	71.1	21	4	US-09-193-542B-19
22	12.2	67.8	19	1	US-08-486-913-2
23	12.2	67.8	19	2	US-08-486-535-2
24	12.2	67.8	19	3	US-08-300-484-2
25	12.2	67.8	19	3	US-08-486-885-2
26	12.2	67.8	19	3	US-08-486-536-2
27	12.2	67.8	19	5	PCT-US95-11234-2

Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 265, App
Sequence 3, Appli
Sequence 3, Appli
Sequence 93, Appli
Sequence 117, App
Sequence 348, App
Sequence 1, Appli
Sequence 348, App
Sequence 22, Appl
Sequence 22, Appl
Sequence 66, Appl
Sequence 101, App
Sequence 101, App
Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-08-529-878B-3
; Sequence 3, Application US/08529878B
; Patent No. 5932556
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; REGULATION OF CD28 EXPRESSION
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Crockett & Fish
; STREET: 3000 S. Augusta Court
; CITY: La Habra
; STATE: California
; COUNTRY: United States of America
; ZIP: 90631
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08529,878B
; FILING DATE: 13-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Fish, Robert D.
; REGISTRATION NUMBER: 33,880
; REFERENCE/DOCKET NUMBER: 213/003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-525-3433
; TELEFAX: 714-525-3303
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-529-878B-3

Query Match 91.1%; Score 16.4; DB 2; Length 18;

Best Local Similarity 94.4%; Pred. No. 1.6e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGAGGGGAGGTGGG 18

Db 1 TTGGAGGGGAGGTGGG 18

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RESULT 2
US-08-529-878B-44
; Sequence 44, Application US/08529878B
; Patent No. 5932556
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Crockett & Fish
; STREET: 3000 S. Augusta Court
; CITY: La Habra
; STATE: California
; COUNTRY: United States of America
; ZIP: 90631
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/529.878B
; FILING DATE: 13-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Fish, Robert D.
; REGISTRATION NUMBER: 33,880
; REFERENCE/DOCKET NUMBER: 213/003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-525-3433
; TELEFAX: 714-525-3303
; TELEX:
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-529-878B-44

Query Match 91.1%; Score 16.4; DB 2; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.6e-02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGAGGTGGGG 18
Db 1 TTGGAGGGGGTGTGGGG 18

RESULT 3
US-08-529-878B-4
; Sequence 4, Application US/08529878B
; Patent No. 5932556
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Crockett & Fish
; STREET: 3000 S. Augusta Court
; CITY: La Habra
; STATE: California
; COUNTRY: United States of America
; ZIP: 90631
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/529.878B
; FILING DATE: 13-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Fish, Robert D.
; REGISTRATION NUMBER: 33,880
; REFERENCE/DOCKET NUMBER: 213/003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-525-3433
; TELEFAX: 714-525-3303
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-529-878B-4

Query Match 91.1%; Score 16.4; DB 2; Length 21;
Best Local Similarity 94.4%; Pred. No. 1.6e-02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGAGGTGGGG 18
Db 4 TTGGAGGGGGTGTGGGG 21

RESULT 4
US-08-529-878B-45
; Sequence 45, Application US/08529878B
; Patent No. 5932556
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Crockett & Fish
; STREET: 3000 S. Augusta Court
; CITY: La Habra
; STATE: California
; COUNTRY: United States of America
; ZIP: 90631
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/529.878B
; FILING DATE: 13-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Fish, Robert D.
; REGISTRATION NUMBER: 33,880
; REFERENCE/DOCKET NUMBER: 213/003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-525-3433
; TELEFAX: 714-525-3303
; TELEX:
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-529-878B-45

Query Match 91.1%; Score 16.4; DB 2; Length 21;
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Best Local Similarity 94.4%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTGAGGGGGAGGTGGGG 18
Db 4 TTGAGGGGGGTGGTGGGG 21

RESULT 5

US-09-487-368A-174
Sequence 174, Application US/09487368A

Patent No. 6261540

GENERAL INFORMATION:

APPLICANT: Lex M. Cowsett

ADDRESSEE: Jacqueline Wyatt

TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION

FILE REFERENCE: RTS-0093

CURRENT APPLICATION NUMBER: US/09/487,368A

CURRENT FILING DATE: 2000-01-18

NUMBER OF SEQ ID NOS: 240

SEQ ID NO 174

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide

US-09-487-368A-174

Query Match 76.7%; Score 13.8; DB 3; Length 20;

Best Local Similarity 88.2%; Pred. No. 1.7e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGGAGGGGGAGGTGGGG 18

Db 1 TGGCCGGGGAGGTGGGG 17

RESULT 6

US-09-629-644A-174

Sequence 174, Application US/09629644A

Patent No. 6492345

GENERAL INFORMATION:

APPLICANT: Lex M. Cowsett

ADDRESSEE: Jacqueline Wyatt

APPLICANT: Susan M. Freier

APPLICANT: Brett P. Monia

APPLICANT: Madeline M. Butler

APPLICANT: Robert McKay

TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION

FILE REFERENCE: ISPH-0478

CURRENT APPLICATION NUMBER: US/09/629,644A

CURRENT FILING DATE: 2000-07-31

PRIOR APPLICATION NUMBER: US 09/487,368

PRIOR FILING DATE: 2000-01-18

NUMBER OF SEQ ID NOS: 242

SEQ ID NO 174

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide

US-09-629-644A-174

Query Match

Best Local Similarity 76.7%; Score 13.8; DB 4; Length 20;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGGAGGGGGAGGTGGGG 18

Db 1 TGGCCGGGGAGGTGGGG 17

RESULT 7

US-09-092-077-45

Sequence 45, Application US/09092077

Patent No. 6194142

GENERAL INFORMATION:

APPLICANT: Moncany, Maurice

ADDRESSEE: Montagnier, Luc

TITLE OF INVENTION: Nucleotide Sequences Derived From The

TITLE OF INVENTION: Genome Of Retroviruses Of The HIV-1, HIV-2 And SIV Type,

TITLE OF INVENTION: And Their Uses In Particular For The Amplification Of The

TITLE OF INVENTION: Genomes Of These Retroviruses And For The In Vitro Diagnosis

TITLE OF INVENTION: Of The Diseases Due To Those Viruses

NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Parabow, Garrett &

ADDRESSEE: Dunner

STREET: 1300 I Street, N.W., Suite 700

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/092,077

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/472,928

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: US 08/160,465

FILING DATE: 02-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 8912371

FILING DATE: 20-SEP-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 8907354

FILING DATE: 06-FEB-1989

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.

REGISTRATION NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 02356.0062-02000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)408-4000

TELEFAX: (202)408-4400

INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-09-092-077-45

Query Match 76.7%; Score 13.8; DB 3; Length 21;

Best Local Similarity 88.2%; Pred. No. 1.7e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGGAGGGGGAGGTGGGG 18

Db 3 TGGAGGGGGAGGTGGGG 19

RESULT 8

US-08-242-664-37

Sequence 37, Application US/08242664

Patent No. 5571937

GENERAL INFORMATION:

APPLICANT: Watanabe, Kyoichi A.

APPLICANT: Ren, Wu-Yun

APPLICANT: Weil, Roger

;; TITLE OF INVENTION: Complementary DNA and Toxins
;; NUMBER OF SEQUENCES: 43
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Cooper & Dunham
;; STREET: 30 Rockefeller Plaza
;; CITY: New York
;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 10112
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch 1.44Mb
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.24
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/242,664
;; FILING DATE: May 12, 1994
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: White, John P.
;; REGISTRATION NUMBER: 28,678
;; REFERENCE/DOCKET NUMBER: 44683
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212-977-9550
;; TELEFAX: 212-664-0525
;; INFORMATION FOR SEQ ID NO: 37:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 19 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
US-08-242-664-37

Query Match 74.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 2.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGAGGGGAGGTGGG 17
Db 5 GGAGGAGGAGGTGGG 19

RESULT 9
US-08-484-138-37
;; Sequence 37, Application US/08484138
;; Patent No. 5652350
;; GENERAL INFORMATION:
;; APPLICANT: Watanabe, Kyoichi A.
;; APPLICANT: Ren, Wu-Yun
;; APPLICANT: Weil, Roger
;; TITLE OF INVENTION: Complementary DNA and Toxins
;; NUMBER OF SEQUENCES: 43
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Cooper & Dunham LLP
;; STREET: 1185 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 10036
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch 1.44Mb
;; COMPUTER: IBM PC
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.24
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/484,138
;; FILING DATE: June 7, 1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: White, John P.
;; REGISTRATION NUMBER: 28,678
;; REFERENCE/DOCKET NUMBER: 44683-Z/JPW/MJG

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212-977-9550
;; TELEFAX: 212-664-0525
;; INFORMATION FOR SEQ ID NO: 37:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 19 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
US-08-484-138-37

Query Match 74.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 2.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGAGGGGAGGTGGG 17
Db 5 GGAGGAGGAGGTGGG 19

RESULT 10
PCT-US95-06379-37
;; Sequence 37, Application PC/TUS9506379
;; GENERAL INFORMATION:
;; APPLICANT: Watanabe, Kyoichi A.
;; APPLICANT: Ren, Wu-Yun
;; APPLICANT: Weil, Roger
;; TITLE OF INVENTION: Complementary DNA and Toxins
;; NUMBER OF SEQUENCES: 43
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Cooper & Dunham LLP
;; STREET: 1185 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 10036
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch 1.44Mb
;; COMPUTER: IBM PC
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.24
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/06379
;; FILING DATE: May 13, 1994
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: White, John P.
;; REGISTRATION NUMBER: 28,678
;; REFERENCE/DOCKET NUMBER: 44683-PCT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212-278-0400
;; TELEFAX: 212-391-0526
;; INFORMATION FOR SEQ ID NO: 37:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 19 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
PCT-US95-06379-37

Query Match 74.4%; Score 13.4; DB 5; Length 19;
Best Local Similarity 93.3%; Pred. No. 2.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGAGGGGAGGTGGG 17
Db 5 GGAGGAGGAGGTGGG 19

RESULT 11
US-09-422-978-9409/c

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; Sequence 9409, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Ballelic markers for use in constructing a high density...
; FILE REFERENCE: GENSER.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 9409
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: downstream amplification primer 99-449 for SEQ 1544, in complement
US-09-422-978-9409

Query Match 74.4%; Score 13.4; DB 4; Length 20;
Best Local Similarity 93.3%; Pred. No. 2.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGAGTGC 15
DB 17 TTGGAGGGGGAGATG 3

RESULT 12
US-08-173-489C-127/c
; Sequence 127, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 127:
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```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; DESCRIPTION: alpha-1-globin gene (accession #
; DESCRIPTION: V00491) nucleotides 827 to 843
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; AUTHORS: Michelson, A M, Orkin, S H.
; TITLE: The 3' untranslated regions
; TITLE: of the duplicated human alpha-globin genes are
; TITLE: unexpectedly divergent
; JOURNAL: Cell
; VOLUME: 22
; PAGES: 371-377
; DATE: 1980
; RELEVANT RESIDUES IN SEQ ID NO: 127 :FROM 1 TO 17
US-08-173-489C-127

Query Match 71.1%; Score 12.8; DB 2; Length 17;
Best Local Similarity 87.5%; Pred. No. 4.3e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGTGGGG 18
DB 16 GGAAGGGGAGGAGGGG 1

RESULT 13
US-09-495-140-26
; Sequence 26, Application US/09495140
; Patent No. 6376182
; GENERAL INFORMATION:
; APPLICANT: CHAO, LEE
; APPLICANT: CHAO, JULIE
; APPLICANT: SONG, QING
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING
; TITLE OF INVENTION: TISSUE KALLIKREIN GENE PROMOTER POLYMORPHISMS WITH TREATMENT
; TITLE OF INVENTION: OF ESSENTIAL HYPERTENSION
; FILE REFERENCE: 19113.0081
; CURRENT APPLICATION NUMBER: US/09/495,140
; CURRENT FILING DATE: 2000-01-31
; EARLIER APPLICATION NUMBER: 09/389,566
; EARLIER FILING DATE: 1999-09-03
; EARLIER APPLICATION NUMBER: 08/856,141
; EARLIER FILING DATE: 1997-05-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. 6376182e =
; OTHER INFORMATION: synthetic construct
US-09-495-140-26

Query Match 71.1%; Score 12.8; DB 4; Length 17;
Best Local Similarity 87.5%; Pred. No. 4.3e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGTGGGG 18
DB 1 GGAGGGGGGGGGGGGGG 16

RESULT 14
US-08-639-501-72
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; Sequence 72, Application US/08639501
; Patent No. 5837492

; GENERAL INFORMATION:

; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Kamb, Alexander
; APPLICANT: Simard, Jacques
; APPLICANT: Couch, Ferguson
; APPLICANT: Rommens, Johanna
; APPLICANT: Weber, Barbara
; TITLE OF INVENTION: Chromosome 13-Linked Breast Cancer
; TITLE OF INVENTION: Susceptibility Gene
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS: 124
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue N.W., Suite 1001
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 22204

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/639,501
; FILING DATE: 29-APR-1996
; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/585,391
; FILING DATE: 11-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/576,559
; FILING DATE: 21-DEC-1995
; APPLICATION NUMBER: US 08/575,359
; FILING DATE: 20-DEC-1995
; APPLICATION NUMBER: US 08/573,779
; FILING DATE: 18-DEC-1995
; ATTORNEY/AGENT INFORMATION:

; NAME: Innen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-116802-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300

; INFORMATION FOR SEQ ID NO: 72:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens

; US-08-639-501-72

Query Match 71.1%; Score 12.8; DB 2; Length 18;
Best Local Similarity 87.5%; Pred. No. 4.3e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGGAGGGGAGGTGG 16

Db 1 TTGGAGAGGAGGTGG 16

RESULT 15

US-09-044-946-72
; Sequence 72, Application US/09044946
; Patent No. 6033857

; GENERAL INFORMATION:

; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Kamb, Alexander
; APPLICANT: Simard, Jacques
; APPLICANT: Couch, Ferguson
; APPLICANT: Rommens, Johanna
; APPLICANT: Weber, Barbara
; TITLE OF INVENTION: Chromosome 13-Linked Breast Cancer
; TITLE OF INVENTION: Susceptibility Gene
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS: 124
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue N.W., Suite 1001
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 22204

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/044,946
; FILING DATE:
; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/639,501
; FILING DATE:
; APPLICATION NUMBER: US 08/576,559
; FILING DATE: 21-DEC-1995
; APPLICATION NUMBER: US 08/575,359
; FILING DATE: 20-DEC-1995
; APPLICATION NUMBER: US 08/573,779
; FILING DATE: 18-DEC-1995
; ATTORNEY/AGENT INFORMATION:

; NAME: Innen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-116802-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300

; INFORMATION FOR SEQ ID NO: 72:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens

; US-09-044-946-72

Query Match 71.1%; Score 12.8; DB 3; Length 18;
Best Local Similarity 87.5%; Pred. No. 4.3e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGGAGGGGAGGTGG 16

Db 1 TTGGAGAGGAGGTGG 16

Search completed: October 27, 2003, 14:03:35
Job time : 41.3143 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 11:25:34 ; Search time 387.943 Seconds
(without alignments)
124.432 Million cell updates/sec

Title: US-09-331-204A-8
Perfect score: 18
Sequence: 1 ttgaggaggaggtggg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1792395 seqs, 1340900451 residues

Total number of hits satisfying chosen parameters: 408622

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:

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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	14.4	80.0	17	12	US-10-303-109A-30
C 2	13.8	76.7	20	9	US-09-854-883-174
C 3	13.4	74.4	17	12	US-10-061-201-1934
C 4	13.4	74.4	17	12	US-10-061-201-1935
C 5	13.4	74.4	17	12	US-10-061-201-1936
C 6	13.4	74.4	19	14	US-10-010-920-67
C 7	13.4	74.4	19	14	US-10-008-721-67
C 8	13.2	73.3	21	9	US-09-828-034-28
C 9	13.2	72.2	20	12	US-10-233-032A-22
C 10	12.8	71.1	17	11	US-09-780-533A-45
C 11	12.8	71.1	17	11	US-09-780-533A-894
C 12	12.8	71.1	17	14	US-10-059-888-26
C 13	12.8	71.1	17	14	US-10-059-888-26
C 14	12.8	71.1	20	9	US-09-854-883-175
C 15	12.8	71.1	20	11	US-09-952-464A-32
C 16	12.8	71.1	20	13	US-10-060-301-34

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17 12.4 68.9 17 12 US-10-238-700-3257 Sequence 3257, Ap
18 12.4 68.9 17 12 US-10-061-201-1933 Sequence 1933, Ap
19 12.4 68.9 17 12 US-10-061-201-1937 Sequence 1937, Ap
20 12.4 68.9 21 11 US-09-382-860-181 Sequence 181, App
21 12.2 67.8 17 9 US-09-866-108-1256 Sequence 1256, Ap
22 12.2 67.8 17 11 US-09-930-423-1590 Sequence 1590, Ap
23 12.2 67.8 17 12 US-09-745-237A-1590 Sequence 1590, Ap
24 12.2 67.8 17 12 US-10-061-201-1956 Sequence 1956, Ap
25 12.2 67.8 20 9 US-09-752-983-265 Sequence 265, App
26 12.2 67.8 20 12 US-10-032-585-5333 Sequence 5333, Ap
27 12 66.7 16 11 US-09-864-636A-2570 Sequence 2570, Ap
28 12 66.7 16 12 US-10-084-839-2570 Sequence 2570, Ap
29 11.8 65.6 16 12 US-10-059-877-22 Sequence 22, Appl
30 11.8 65.6 16 14 US-10-059-888-22 Sequence 22, Appl
31 11.8 65.6 17 11 US-09-780-533A-893 Sequence 893, App
32 11.8 65.6 17 11 US-09-780-533A-895 Sequence 895, App
33 11.8 65.6 17 11 US-09-930-423-1591 Sequence 1591, Ap
34 11.8 65.6 17 11 US-09-740-332-1833 Sequence 1833, Ap
35 11.8 65.6 17 12 US-09-745-237A-1591 Sequence 1591, Ap
36 11.8 65.6 17 12 US-09-817-879-1833 Sequence 1833, Ap
37 11.8 65.6 18 14 US-10-265-689-40 Sequence 40, Appl
38 11.8 65.6 19 12 US-10-205-309-49 Sequence 49, Appl
39 11.8 65.6 19 12 US-10-205-309-374 Sequence 374, App
40 11.8 65.6 20 10 US-09-874-162A-22 Sequence 22, Appl
41 11.8 65.6 20 11 US-09-948-002-30 Sequence 30, Appl
42 11.8 65.6 20 12 US-10-024-369-53 Sequence 53, Appl
43 11.8 65.6 20 12 US-10-024-369-33 Sequence 33, Appl
44 11.8 65.6 21 11 US-09-932-300-10 Sequence 10, Appl
45 11.8 65.6 21 11 US-09-932-300-24 Sequence 24, Appl
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ALIGNMENTS

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RESULT 1
US-10-303-109A-30/c
; Sequence 30, Application US/10303109A
; Publication No. US20030194726A1
; GENERAL INFORMATION:
; APPLICANT: BOLCHAKOVA, Elena
; APPLICANT: ROZZELLE, James
; TITLE OF INVENTION: Thermus oshimai Nucleic Acid Polymerases
; FILE REFERENCE: 477705
; CURRENT APPLICATION NUMBER: US/10/303,109A
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/334,798
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 30
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Thermus oshimai
US-10-303-109A-30
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Query Match 80.0%; Score 14.4; DB 12; Length 17;
Best Local Similarity 93.8%; Pred. No. 6.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 2 TGGAGGGGAGGTGGG 17
```

```
Db 16 TGGAGGTGGAGGTGGG 1
```

```
RESULT 2
US-09-854-883-174
; Sequence 174, Application US/09854883
; Patent No. US20020055479A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; APPLICANT: Brett P. Morla
```



```
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1936
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-1936

Query Match      74.4%; Score 13.4; DB 12; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 GAGGGGGAGGTGGG 18
Db      15 GAGGGGGAGGTGGG 1

RESULT 6
US-10-010-920-67
; Sequence 67, Application US/10010920
; Publication No. US20030027165A1
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; TITLE OF INVENTION: Alternatively spliced polk nucleotide and amino acid sequences
; FILE REFERENCE: 98,723-E3
; CURRENT APPLICATION NUMBER: US/10/010,920
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/254,649
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer ON-DHFR-F1
US-10-010-920-67

Query Match      74.4%; Score 13.4; DB 14; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 TGGAGGGGAGGTGG 16
Db      5 TGGAGGAGGAGGTGG 19

RESULT 7
US-10-008-721-67
; Sequence 67, Application US/10008721
; Publication No. US20030082745A1
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; TITLE OF INVENTION: TNF-Inducible Promoters and Methods for Using
; FILE REFERENCE: 98,723-E1
; CURRENT APPLICATION NUMBER: US/10/008,721
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/254,649
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense PCR primer for CC3 promoter (spec Table IIIa)
US-10-008-721-67
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer ON-DHFR-F1
US-10-008-721-67

Query Match      74.4%; Score 13.4; DB 14; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 TGGAGGGGAGGTGG 16
Db      5 TGGAGGAGGAGGTGG 19

RESULT 8
US-09-828-034-28/c
; Sequence 28, Application US/09828034
; Patent No. US20020064771A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Weidong
; APPLICANT: Hong, Zhi
; TITLE OF INVENTION: HCV REPLICASE COMPLEXES
; FILE REFERENCE: IN01165
; CURRENT APPLICATION NUMBER: US/09/828,034
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: U.S. 60/195,852
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
US-09-828-034-28

Query Match      73.3%; Score 13.2; DB 9; Length 21;
Best Local Similarity 83.3%; Pred. No. 1.9e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 TTGGAGGGGAGGTGGG 18
Db      20 TTGGAGGAGGAGGAGGAG 3

RESULT 9
US-10-233-032A-22
; Sequence 22, Application US/10233032A
; Publication No. US20030157704A1
; GENERAL INFORMATION:
; APPLICANT: Poole, Jason
; APPLICANT: Roninson, Igor
; APPLICANT: Chang, Bey-Din
; TITLE OF INVENTION: REAGENTS AND METHODS FOR IDENTIFYING AND MODULATING
; FILE REFERENCE: 01-1156-A
; CURRENT APPLICATION NUMBER: US/10/233,032A
; CURRENT FILING DATE: 2003-02-12
; PRIOR APPLICATION NUMBER: US 09/861,925
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/265,840
; PRIOR FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; FEATURE:
; OTHER INFORMATION: Antisense PCR primer for CC3 promoter (spec Table IIIa)
US-10-233-032A-22
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Query Match 72.2%; Score 13; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+04; Indels 0;
Matches 13; Conservative 0; Mismatches 0; Gaps 0;

QY 5 AGGGGAGGTGGG 17
|||||
Db 1 AGGGGAGGTGGG 13

RESULT 10

US-09-780-533A-45/c
; Sequence 45, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH800.878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
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; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-45

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Best Local Similarity 87.5%; Pred. No. 2.9e+04; Indels 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGAGGTGGG 18
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Db 16 GGAGGGGAGGTGGG 1

RESULT 11

US-09-780-533A-894/c
; Sequence 894, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH800.878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 894
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-894

Query Match 71.1%; Score 12.8; DB 11; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.9e+04; Indels 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGAGGTGGG 18
|||||

Db 17 GGAGGGGAGGTGGG 2

RESULT 12

US-10-059-877-26
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; Publication No. US20030157490A1
; GENERAL INFORMATION:
; APPLICANT: CHAO, LEE
; APPLICANT: CHAO, JULIE
; APPLICANT: SONG, QING
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING
; TITLE OF INVENTION: TISSUE KALLIKREIN GENE PROMOTER POLYMORPHISMS WITH ESSENTIAL
; FILE REFERENCE: 19113.0081U2
; CURRENT APPLICATION NUMBER: US/10/059,877
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: 09/495,140
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 09/389,566
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 08/856,141
; PRIOR FILING DATE: 1997-05-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030157490A1e =
US-10-059-877-26

Query Match 71.1%; Score 12.8; DB 12; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.9e+04; Indels 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGAGGTGGG 18
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Db 1 GGAGGGGAGGTGGG 16

RESULT 13

US-10-059-888-26
; Sequence 26, Application US/10059888
; Publication No. US20030025892A1
; GENERAL INFORMATION:
; APPLICANT: CHAO, LEE
; APPLICANT: SONG, QING
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING
; TITLE OF INVENTION: TISSUE KALLIKREIN GENE PROMOTER POLYMORPHISMS WITH ESSENTIAL
; FILE REFERENCE: 19113.0081U2
; CURRENT APPLICATION NUMBER: US/10/059,888
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: 09/495,140
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 09/389,566
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 08/856,141
; PRIOR FILING DATE: 1997-05-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030025892A1e =
US-10-059-888-26

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Best Local Similarity 87.5%; Pred. No. 2.9e+04;
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Db 1 GGAGGGGGGGGGGG 16

RESULT 14
US-09-854-883-175
; Sequence 175, Application US/09854883
; Patent No. US20020055479A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Robert McKay
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTPIB EXPRESSION
; FILE REFERENCE: ISPH-0576
; CURRENT APPLICATION NUMBER: US/09/854,883
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/629,644
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/487,368
; PRIOR FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 389
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-854-883-175

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Best Local Similarity 87.5%; Pred. No. 2.8e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Best Local Similarity 87.5%; Pred. No. 2.8e+04;
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; Sequence 32, Application US/09952464A
; Publication No. US20030077587A1
; GENERAL INFORMATION:
; APPLICANT: Stone, Edwin M.
; APPLICANT: Sheffield, Val C.
; APPLICANT: Alward, Wallace L.M.
; APPLICANT: Fingert, John
; TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
; FILE REFERENCE: 21087.0017U11
; CURRENT APPLICATION NUMBER: US/09/952,464A
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: 09/473,273
; PRIOR FILING DATE: 1999-12-28
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; PRIOR FILING DATE: 1999-08-04
; PRIOR APPLICATION NUMBER: 09/056,285
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: 08/822,999
; PRIOR FILING DATE: 1997-03-21
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	18	100.0	18	19	US-09-331-204A-8
3	16.4	91.1	18	8	US-08-387-041A-3
4	16.4	91.1	18	19	US-09-331-204-1

5	16.4	91.1	18	19	US-09-331-204A-4	Sequence 4, Appl
6	16.4	91.1	18	19	US-09-331-204A-7	Sequence 7, Appl
7	16.4	91.1	18	33	US-09-786-436-17	Sequence 17, Appl
8	16.4	91.1	18	33	US-09-786-436-42	Sequence 42, Appl
C	9	16.4	91.1	18	US-09-331-204-4	Sequence 4, Appl
10	16.4	91.1	21	8	US-08-387-041A-4	Sequence 4, Appl
11	16.4	91.1	21	19	US-09-331-204-6	Sequence 6, Appl
12	16.4	91.1	21	19	US-09-331-204A-6	Sequence 6, Appl
13	15.4	85.6	19	50	US-10-310-188-47426	Sequence 47426, A
14	15	83.3	18	50	US-10-310-188-38927	Sequence 38927, A
C	15	14.8	82.2	22	US-09-979-666B-79	Sequence 79, Appl
C	16	14.4	80.0	17	PCT-US02-29103-30	Sequence 30, Appl
C	17	14.4	80.0	17	PCT-US02-37657-51	Sequence 51, Appl
C	18	14.4	80.0	17	PCT-US02-37764-30	Sequence 30, Appl
C	19	14.4	80.0	17	US-09-546-745A-1942	Sequence 1942, Ap
C	20	14.4	80.0	17	US-10-302-817A-51	Sequence 51, Appl
C	21	14.4	80.0	17	US-10-303-109A-30	Sequence 30, Appl
C	22	14.4	80.0	22	US-10-310-188-47706	Sequence 47706, A
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31	13.8	76.7	20	51	US-10-360-510-174	Sequence 174, App
32	13.8	76.7	21	9	US-08-472-928B-45	Sequence 45, Appl
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C	37	13.4	74.4	17	US-10-061-201-1935	Sequence 1935, Ap
C	38	13.4	74.4	17	US-10-061-201-1936	Sequence 1936, Ap
C	39	13.4	74.4	17	US-60-328-205-1934	Sequence 1934, Ap
C	40	13.4	74.4	17	US-60-328-205-1935	Sequence 1935, Ap
C	41	13.4	74.4	17	US-60-328-205-1936	Sequence 1936, Ap
C	42	13.4	74.4	18	US-10-266-090-45765	Sequence 45765, A
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ALIGNMENTS

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RESULT 1
US-09-331-204-5
; Sequence 5, Application US/09331204
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert
; TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN
; TITLE OF INVENTION: IMMUNE RESPONSE
; FILE REFERENCE: ICNSequence
; CURRENT APPLICATION NUMBER: US/09/331,204
; CURRENT FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US97/23927
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; TYPE: DNA
; LENGTH: 18
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: An oligomer
; OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic
; OTHER INFORMATION: acid. This term includes oligomers consisting of
; OTHER INFORMATION: naturally occurring bases, sugars and intersugar (
US-09-331-204-5

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Query Match	100.0%	Score 18;	DB 19;	Length 18;
Best Local Similarity	100.0%	Pred. No.	5.1e+03;	

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB       1 TTGAGGGGGAGGTGGG 18
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RESULT 2
US-09-331-204A-8
; Sequence 8, Application US/09331204A
; GENERAL INFORMATION:
; APPLICANT: ICN Pharmaceuticals, Inc.
; APPLICANT: Tam, Robert
; TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Response
; FILE REFERENCE: 216/013-US1
; CURRENT APPLICATION NUMBER: US/09/331,204A
; CURRENT FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US97/23927
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 18
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-331-204A-8

Query Match 100.0%; Score 18; DB 19; Length 18;
Best Local Similarity 100.0%; Pred No, 5.le+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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3  Sequence 3, Application US/08387041A
4  GENERAL INFORMATION:
5  APPLICANT: Tam, Robert C.
6  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATION
7  OF CD28 EXPRESSION
8  NUMBER OF SEQUENCES: 41
9  CORRESPONDENCE ADDRESS:
10 ADDRESSSEE: Pennie & Edmonds
11 CITY: New York
12 STATE: New York
13 COUNTRY: United States of America
14 Zip: 10036
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: Patent In Release #1.0, Version #1.30
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08/387.041A
22 FILING DATE: 02-FEB-1995
23 CLASSIFICATION: 514
24 ATTORNEY/AGENT INFORMATION:
25 NAME: Hailuin, Albert P.
26 REGISTRATION NUMBER: 25,227
27 REFERENCE/DOCKET NUMBER: 8250-011
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: 415-854-3660
30 TELEFAX: 415-854-3694
31 TELEX: 66141 PENNIE
32 INFORMATION FOR SEQ ID NO: 3:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 18 base pairs
35 TYPE: nucleic acid
36 STRANDEDNESS: unknown

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TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-387-041A-3

Query Match 91.1%; Score 16.4; DB 8; Length 18;
Best Local Similarity 94.4%; Pred. No. 2.1e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGAGGGGGAGGTGGGG 18
Db 1 TTGAGGGGGGTGGTGGGG 18

RESULT 4

US-09-331-204-1
; Sequence 1, Application US/09331204
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert
; TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN
; FILE REFERENCE: ICN Sequence
; CURRENT APPLICATION NUMBER: US/09/331,204
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US97/23927
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence. An oligomer
; OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic
; OTHER INFORMATION: acid including oligomers consisting of naturally
; OTHER INFORMATION: occurring bases, sugars and intersugar
US-09-331-204-1

Query Match 91.1%; Score 16.4; DB 19; Length 18;
Best Local Similarity 94.4%; Pred. No. 2.1e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGAGGGGGAGGTGGGG 18
Db 1 TTGAGGGGGGTGGTGGGG 18

RESULT 5

US-09-331-204A-4
; Sequence 4, Application US/09331204A
; GENERAL INFORMATION:
; APPLICANT: ICN Pharmaceuticals, Inc.
; APPLICANT: Tam, Robert
; TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Respo
; FILE REFERENCE: 216/013-US1
; CURRENT APPLICATION NUMBER: US/09/331,204A
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US97/23927
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 18
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-331-204A-4

Query Match 91.1%; Score 16.4; DB 19; Length 18;
Best Local Similarity 94.4%; Pred. No. 2.1e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGAGGGGGAGGTGGGG 18
Db 1 TTGAGGGGGGTGGTGGGG 18

Db 1 TTGAGGGGGGTGGTGGGG 18

RESULT 6

US-09-331-204A-7
; Sequence 7, Application US/09331204A
; GENERAL INFORMATION:
; APPLICANT: ICN Pharmaceuticals, Inc.
; APPLICANT: Tam, Robert
; TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Resp
; FILE REFERENCE: 216/013-US1
; CURRENT APPLICATION NUMBER: US/09/331,204A
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US97/23927
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 18
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-331-204A-7

Query Match 91.1%; Score 16.4; DB 19; Length 18;
Best Local Similarity 94.4%; Pred. No. 2.1e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGAGGGGGAGGTGGGG 18
Db 1 TTGAGGGGGGTGGTGGGG 18

RESULT 7

US-09-786-436-17
; Sequence 17, Application US/09786436
; GENERAL INFORMATION:
; APPLICANT: Wagner, Hermann
; APPLICANT: Lipford, Grayson
; APPLICANT: Heeg, Klaus
; TITLE OF INVENTION: G-Motif Oligonucleotides and Uses
; FILE REFERENCE: C1041/7010 (AWS)
; CURRENT APPLICATION NUMBER: US/09/786,436
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: PCT/EP99/06502
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-09-786-436-17

Query Match 91.1%; Score 16.4; DB 33; Length 18;
Best Local Similarity 94.4%; Pred. No. 2.1e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGAGGGGGAGGTGGGG 18
Db 1 TTGAGGGGGGTGGTGGGG 18

RESULT 8

US-09-786-436-42/c
; Sequence 42, Application US/09786436
; GENERAL INFORMATION:
; APPLICANT: Wagner, Hermann
; APPLICANT: Lipford, Grayson
; APPLICANT: Heeg, Klaus
; TITLE OF INVENTION: G-Motif Oligonucleotides and Uses

```
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: C1041/7010 (AWS)
; CURRENT APPLICATION NUMBER: US/09/786,436
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: PCI/EP99/06502
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-09-786-436-42

Query Match          91.1%; Score 16.4; DB 33; Length 18;
Best Local Similarity 94.4%; Pred. No. 2.1e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGAGGTGGGG 18
Db 18 TTGGAGGGGGTGTGGGG 1

RESULT 9
US-09-331-204-4
; Sequence 4, Application US/09331204
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert
; TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN
; FILE REFERENCE: ICNSequence
; CURRENT APPLICATION NUMBER: US/09/331,204
; CURRENT FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US97/23927
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: An oligomer
; OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic
; OTHER INFORMATION: acid. This term includes oligomers consisting of
; OTHER INFORMATION: naturally occurring bases, sugars and intersugar (
US-09-331-204-4

Query Match          91.1%; Score 16.4; DB 19; Length 19;
Best Local Similarity 94.4%; Pred. No. 2.1e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGAGGTGGGG 18
Db 1 TTGGAGGGGGAGGAGGGG 18

RESULT 10
US-08-387-041A-4
; Sequence 4, Application US/08387041A
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATION
; TITLE OF INVENTION: OF CD28 EXPRESSION
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
```

```
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,041A
; FILING DATE: 02-FEB-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8250-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-387-041A-4

Query Match          91.1%; Score 16.4; DB 8; Length 21;
Best Local Similarity 94.4%; Pred. No. 2.1e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGAGGTGGGG 18
Db 4 TTGGAGGGGGTGTGGGG 21

RESULT 11
US-09-331-204-6
; Sequence 6, Application US/09331204
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert
; TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN
; FILE REFERENCE: ICNSequence
; CURRENT APPLICATION NUMBER: US/09/331,204
; CURRENT FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US97/23927
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: An oligomer
; OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic
; OTHER INFORMATION: acid. This term includes oligomers consisting of
; OTHER INFORMATION: naturally occurring bases, sugars and intersugar (
US-09-331-204-6

Query Match          91.1%; Score 16.4; DB 19; Length 21;
Best Local Similarity 94.4%; Pred. No. 2.1e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGAGGTGGGG 18
Db 4 TTGGAGGGGGTGTGGGG 21

RESULT 12
US-09-331-204A-6
; Sequence 6, Application US/09331204A
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; GENERAL INFORMATION:
; APPLICANT: ICN Pharmaceuticals, Inc.
; TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Response
; FILE REFERENCE: 216/013-US1
; CURRENT APPLICATION NUMBER: US/09/331,204A
; CURRENT FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US97/23927
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 21
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-331-204A-6

Query Match          91.1%; Score 16.4; DB 19; Length 21;
Best Local Similarity 94.4%; Pred. No. 2.1e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGAGGGGAGGTGGG 18
Db 4 TTGGAGGGGAGGTGGG 21

RESULT 13
US-10-310-188-47426
; Sequence 47426, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47426
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-47426

Query Match          85.6%; Score 15.4; DB 50; Length 19;
Best Local Similarity 94.1%; Pred. No. 4.9e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGGAGGGGAGGTGGG 18
Db 3 TGGAGGGGAGGTGGG 19

RESULT 14
US-10-310-188-38927
; Sequence 38927, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38927
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-38927

Query Match          83.3%; Score 15; DB 50; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.9e+04;
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGAGGGGAGGTGGG 17
Db 3 GGAGGGGAGGTGGG 17

RESULT 15
US-09-979-666B-79
; Sequence 79, Application US/09979666B
; GENERAL INFORMATION:
; APPLICANT: TACHAS, GEORGE
; TITLE OF INVENTION: INHIBITION OF GASTRIC ACID PRODUCTION AND/OR SECRETION
; FILE REFERENCE: 47-162
; CURRENT APPLICATION NUMBER: US/09/979,666B
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
; OTHER INFORMATION: Synthetic antisense oligonucleotide, can be
; OTHER INFORMATION: RNA, DNA or chimera
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: antisense oligonucleotide, can be RNA, DNA
; OTHER INFORMATION: or chimera
US-09-979-666B-79

Query Match          82.2%; Score 14.8; DB 42; Length 22;
Best Local Similarity 81.2%; Pred. No. 8.3e+04;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGAGGGGAGGTGGG 17
Db 2 TGGAGGGGAGGTGGG 17

Search completed: October 27, 2003, 17:52:54
Job time : 2357.29 secs
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GenCore version 5.1.6
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CM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 11:09:34 ; Search time 307.029 Seconds
(without alignments)
97.777 Million cell updates/sec

Title: US-09-331-204A-8

Perfect score: 18

Sequence: 1 ttgagggggagggtggggg 18

Scoring table: IDENTITY NUC

Gapop 10.0 ; Gapext 1.0

Searched: 2231628 seqs, 833900706 residues

Total number of hits satisfying chosen parameters: 264402

Minimum DB seq length: 0

Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents NA New: *

- 1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
- 2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
- 3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
- 4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
- 5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
- 6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
- 7: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15.4	85.6	19	1	PCT-US02-38216-47426
2	15	83.3	18	1	PCT-US02-38216-38927
3	14.4	80.0	21	1	PCT-US03-26780-1166
4	14.4	80.0	22	1	PCT-US02-38216-47706
5	13.8	76.7	19	1	PCT-US02-38216-26651
6	13.8	76.7	20	5	US-09-629-644A-174
7	13.8	76.7	21	1	PCT-US02-38216-51847
8	13.4	74.4	18	1	PCT-US02-38216-6227
9	13.4	74.4	18	1	PCT-US02-38216-25860
10	13.4	74.4	18	1	PCT-US02-38216-38977
11	13.4	74.4	21	1	PCT-US02-38216-51829
12	13.2	73.3	20	1	PCT-US02-38216-36515
13	13.2	73.3	22	1	PCT-US02-38216-48159
14	13	72.2	19	1	PCT-US02-38216-25810
15	13	72.2	19	1	PCT-US02-38216-54492
16	13	72.2	19	1	PCT-US02-38216-64684
17	13	72.2	21	1	PCT-US02-38216-41829
18	12.8	71.1	16	1	PCT-US02-38216-18366
19	12.8	71.1	16	1	PCT-US02-38216-39032
20	12.8	71.1	17	1	PCT-US02-38216-14773
21	12.8	71.1	17	1	PCT-US02-38216-14816
22	12.8	71.1	17	1	PCT-US02-38216-38911
23	12.8	71.1	18	1	PCT-US02-38216-6229
24	12.8	71.1	18	1	PCT-US02-38216-9731
25	12.8	71.1	18	1	PCT-US02-38216-18298
26	12.8	71.1	18	1	PCT-US02-38216-39006

27	12.8	71.1	18	1	PCT-US02-38216-39031	Sequence 39031, A
28	12.8	71.1	18	1	PCT-US02-38216-39102	Sequence 39102, A
29	12.8	71.1	18	1	PCT-US02-38216-41647	Sequence 41647, A
30	12.8	71.1	18	1	PCT-US02-38216-51842	Sequence 51842, A
31	12.8	71.1	18	1	PCT-US02-38216-58279	Sequence 58279, A
32	12.8	71.1	18	1	PCT-US02-38216-60182	Sequence 60182, A
33	12.8	71.1	18	1	PCT-US02-38216-61077	Sequence 61077, A
34	12.8	71.1	18	1	PCT-US02-38216-61101	Sequence 61101, A
35	12.8	71.1	18	1	PCT-US02-38216-72811	Sequence 72811, A
36	12.8	71.1	19	1	PCT-US02-38216-10778	Sequence 10778, A
37	12.8	71.1	19	1	PCT-US02-38216-18422	Sequence 18422, A
38	12.8	71.1	19	1	PCT-US02-38216-38912	Sequence 38912, A
39	12.8	71.1	19	1	PCT-US02-38216-38943	Sequence 38943, A
40	12.8	71.1	19	1	PCT-US02-38216-46976	Sequence 46976, A
41	12.8	71.1	20	1	PCT-US02-38216-14886	Sequence 14886, A
42	12.8	71.1	20	1	PCT-US02-38216-18227	Sequence 18227, A
43	12.8	71.1	20	1	PCT-US02-38216-18520	Sequence 18520, A
44	12.8	71.1	20	1	PCT-US02-38216-26672	Sequence 26672, A
45	12.8	71.1	20	1	PCT-US02-38216-41837	Sequence 41837, A

ALIGNMENTS

RESULT 1
PCT-US02-38216-47426
; Sequence 47426, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 35002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47426
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-47426

Query Match 85.6%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 5.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 TGGAGGGGGAGGTGGGG 18
Db 3 TGGAGGGGGAGGTGGGG 19

RESULT 2
PCT-US02-38216-38927
; Sequence 38927, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 35002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38927
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-38927

Query Match 83.3%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGAGGGGAGGTGGG 17
| | | | | | | | | |
DB 3 GGAGGGGAGGTGGG 17

RESULT 3
PCT-US03-26780-1166
; Sequence 1166, Application PC/TUS0326780
; GENERAL INFORMATION:
; APPLICANT: FIVEPRIME THERAPEUTICS, INC.
; TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF
; TITLE OF INVENTION: THEIR USE
; FILE REFERENCE: 08940.0014-00304
; CURRENT APPLICATION NUMBER: PCT/US03/26780
; CURRENT FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: 60/406,616
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,579
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,655
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,642
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,640
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,588
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,576
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,646
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,666
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/406,653
; PRIOR FILING DATE: 2002-08-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3700
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1166
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US03-26780-1166

Query Match 80.0%; Score 14.4; DB 1; Length 21;
Best Local Similarity 93.8%; Pred. No. 1.3e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGGGAGGTGGG 18
| | | | | | | | | |
DB 1 GGAGGGGAGGTGGG 16

RESULT 4
PCT-US02-38216-47706
; Sequence 47706, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47706
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-47706

Query Match 80.0%; Score 14.4; DB 1; Length 22;
Best Local Similarity 93.8%; Pred. No. 1.3e+04;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 GGAGGGGAGGTGGG 18
| | | | | | | | | |
DB 1 GGAGGGGAGGTGGG 16

RESULT 5
PCT-US02-38216-26651/c
; Sequence 26651, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26651
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-26651

Query Match 76.7%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.2e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGAGGGGAGGTGGG 18
| | | | | | | | | |
DB 18 TGGAGGTGGAGGTGGG 2

RESULT 6
US-09-629-644A-174
; Sequence 174, Application US/09629644A
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freler
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Robert McKay
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTPIB EXPRESSION
; FILE REFERENCE: ISPH-0478
; CURRENT APPLICATION NUMBER: US/09/629,644A
; CURRENT FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/487,368
; PRIOR FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 242
; SEQ ID NO 174
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-629-644A-174

Query Match 76.7%; Score 13.8; DB 5; Length 20;
Best Local Similarity 88.2%; Pred. No. 2.2e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGAGGGGAGGTGGG 18
| | | | | | | | | |
DB 1 TGGCCGGGAGGTGGG 17

RESULT 7
PCT-US02-38216-51847
; Sequence 51847, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD

<p> ; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY ; TITLE OF INVENTION: GENES AND USES THEREOF ; FILE REFERENCE: 55002 ; CURRENT APPLICATION NUMBER: PCT/US02/38216 ; CURRENT FILING DATE: 2002-11-12 ; NUMBER OF SEQ ID NOS: 86841 ; SOFTWARE: PatentIn version 3.2 ; SEQ ID NO 51847 ; LENGTH: 21 ; TYPE: DNA ; ORGANISM: Homo sapiens PCT-US02-38216-51847 </p>		<p> 76.7%; Score 13.8; DB 1; Length 21; Best Local Similarity 88.2%; Pred. No. 2.2e+04; Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0; </p>
Qy	2 TGGAGGGGGAGGTGGGG 18 	
Db	4 TGGTGGGGCGGTGGGG 20 	
<p> RESULT 8 PCT-US02-38216-6227/c ; Sequence 6227, Application PC/TUS0238216 ; GENERAL INFORMATION: ; APPLICANT: Rosetta Genomics LTD ; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY ; FILE REFERENCE: 55002 ; CURRENT APPLICATION NUMBER: PCT/US02/38216 ; CURRENT FILING DATE: 2002-11-12 ; NUMBER OF SEQ ID NOS: 86841 ; SOFTWARE: PatentIn version 3.2 ; SEQ ID NO 6227 ; LENGTH: 18 ; TYPE: DNA ; ORGANISM: Homo sapiens PCT-US02-38216-6227 </p>		
<p> Query Match 74.4%; Score 13.4; DB 1; Length 18; Best Local Similarity 93.3%; Pred. No. 3e+04; Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0; </p>		
Qy	3 GGAGGGGGAGGTGGG 17 	
Db	15 GGAGGGGGAGGAGGG 1 	
<p> RESULT 9 PCT-US02-38216-25860/c ; Sequence 25860, Application PC/TUS0238216 ; GENERAL INFORMATION: ; APPLICANT: Rosetta Genomics LTD ; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY ; FILE REFERENCE: 55002 ; CURRENT APPLICATION NUMBER: PCT/US02/38216 ; CURRENT FILING DATE: 2002-11-12 ; NUMBER OF SEQ ID NOS: 86841 ; SOFTWARE: PatentIn version 3.2 ; SEQ ID NO 25860 ; LENGTH: 18 ; TYPE: DNA ; ORGANISM: Homo sapiens PCT-US02-38216-25860 </p>		
<p> Query Match 74.4%; Score 13.4; DB 1; Length 18; Best Local Similarity 93.3%; Pred. No. 3e+04; Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0; </p>		
Qy	3 GGAGGGGGAGGTGGG 17 	

PCT-US02-38216-36515

Query Match 73.3%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.6e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTGGAGGGGAGGTGGGG 18
| | | | | | | | | | | | | | | | | | | |
Db 2 TTGGGAGTGAGGTGGGG 19
| | | | | | | | | | | | | | | | | | | |

RESULT 13

PCT-US02-38216-18159
; Sequence 18159, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18159
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-18159

Query Match 73.3%; Score 13.2; DB 1; Length 22;
Best Local Similarity 83.3%; Pred. No. 3.5e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTGGAGGGGAGGTGGGG 18
| | | | | | | | | | | | | | | | | | | |
Db 1 TGGGAGGGGAGGAAGGG 18
| | | | | | | | | | | | | | | | | | | |

RESULT 14

PCT-US02-38216-25810/c
; Sequence 25810, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25810
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-25810

Query Match 72.2%; Score 13; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGGGAGGTGGGG 18
| | | | | | | | | | | | | | | | | | | |
Db 14 GGGGAGGTGGGG 2
| | | | | | | | | | | | | | | | | | | |

RESULT 15

PCT-US02-38216-64492/c
; Sequence 64492, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002

; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 64492
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-64492

Query Match 72.2%; Score 13; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGGGAGGTGGGG 18
| | | | | | | | | | | | | | | | | | | |
Db 18 GGGGAGGTGGGG 6
| | | | | | | | | | | | | | | | | | | |

Search completed: October 27, 2003, 18:22:55
Job time : 307.029 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:29 ; Search time 250.743 Seconds
(without alignments)
1957.844 Million cell updates/sec

Title: US-09-331-204A-13
Perfect score: 12
Sequence: 1 ggggtggtggg 12

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 681044

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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2: gb_hg.*
3: gb_in.*
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14: gb_vi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_on.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vi.*
30: em_hg_hum.*
31: em_hg_inv.*
32: em_hg_other.*
33: em_hg_mus.*
34: em_hg_pln.*
35: em_hg_rtd.*
36: em_hg_mam.*
37: em_hg_vrt.*
38: em_sy.*
39: em_hgo_hum.*
40: em_hgo_mus.*
41: em_hgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	12	100.0	18	6	AX023402	AX023402 Sequence
2	12	100.0	18	6	AX023427	AX023427 Sequence
C 3	11	91.7	17	6	A25058	A25058 Nucleobrote
4	11	91.7	17	6	AR168836	AR168836 Sequence
5	11	91.7	17	6	AR168838	AR168838 Sequence
6	11	91.7	17	6	AR168839	AR168839 Sequence
7	11	91.7	17	6	AR200305	AR200305 Sequence
8	11	91.7	17	6	AR200307	AR200307 Sequence
9	11	91.7	17	6	AR200308	AR200308 Sequence
10	11	91.7	17	6	AR262436	AR262436 Sequence
11	11	91.7	17	6	AR262438	AR262438 Sequence
12	11	91.7	17	6	AR262439	AR262439 Sequence
13	11	91.7	17	6	AX284071	AX284071 Sequence
14	11	91.7	17	6	AR078333	AR078333 Sequence
15	11	91.7	20	6	AR092032	AR092032 Sequence
C 16	11	91.7	20	6	AR112167	AR112167 Sequence
C 17	11	91.7	20	6	AR149209	AR149209 Sequence
18	11	91.7	20	6	AR173053	AR173053 Sequence
19	11	91.7	20	6	AX298761	AX298761 Sequence
20	11	91.7	21	6	AR168785	AR168785 Sequence
21	11	91.7	21	6	AR200254	AR200254 Sequence
22	11	91.7	21	6	AR262386	AR262386 Sequence
23	11	91.7	21	6	I27779	I27779 Sequence 11
C 24	10.4	86.7	15	6	AX572880	AX572880 Sequence
25	10.4	86.7	15	6	I72532	I72532 Sequence 2
C 26	10.4	86.7	17	6	AX214607	AX214607 Sequence
C 27	10.4	86.7	17	6	AX215490	AX215490 Sequence
C 28	10.4	86.7	17	6	AX215491	AX215491 Sequence
C 29	10.4	86.7	17	6	AX215492	AX215492 Sequence
C 30	10.4	86.7	17	6	AX215493	AX215493 Sequence
31	10.4	86.7	17	6	AX673765	AX673765 Sequence
C 32	10.4	86.7	17	6	AX728115	AX728115 Sequence
33	10.4	86.7	18	6	A87857	A87857 Sequence 5
34	10.4	86.7	18	6	A89824	A89824 Sequence 5
35	10.4	86.7	18	6	AR002274	AR002274 Sequence
36	10.4	86.7	18	6	AR053125	AR053125 Sequence
C 37	10.4	86.7	18	6	AX117823	AX117823 Sequence
38	10.4	86.7	18	6	AX599746	AX599746 Sequence
39	10.4	86.7	18	6	BD065370	BD065370 An antise
40	10.4	86.7	20	6	AR313443	AR313443 Sequence
41	10.4	86.7	20	6	AX418779	AX418779 Sequence
C 42	10.4	86.7	20	6	AX440601	AX440601 Sequence
43	10.4	86.7	20	6	BD000527	BD000527 Method fo
C 44	10.4	86.7	20	6	E59330	E59330 Method for
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ALIGNMENTS

RESULT 1
AX023402
LOCUS AX023402 18 bp DNA linear PAT 15-SEP-2000
DEFINITION Sequence 17 from Patent WO0014217.
ACCESSION AX023402
VERSION AX023402.1 GI:10183802
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Lipford,G.B., Heeg,K. and Wagner,H.
TITLE G-motif oligonucleotides and uses thereof
JOURNAL Patent: WO 0014217-A 17 16-MAR-2000;
LIPFORD GRAYSON B (DE) ; HEEG KLAUS (DE) ; WAGNER HERMANN (DE) ;

Pred. No. is the number of results predicted by chance to have a

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ACCESSION ARI68839
VERSION ARI68839.1 GI:17904968
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Rando,R.F., Ojwang,J.O., Hogan,M.E., Wallace,T.L. and Cossum,P.A.
TITLE Anti-viral guanosine-rich tetrad forming oligonucleotides
JOURNAL Patent: US 628042-A 65 11-SEP-2001;
FEATURES Location/Qualifiers
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source /organism="unknown"
BASE COUNT 0 a 0 c 12 g 4 t 1 others
ORIGIN

Query Match 91.7%; Score 11; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGG 11
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Db 6 GGGGTGGTGGG 16

RESULT 7
ACCESSION AR200305
LOCUS Sequence 62 from patent US 6355785.
DEFINITION AR200305 linear PAT 20-APR-2002
ACCESSION AR200305
VERSION AR200305.1 GI:20250379
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Rando,R.F., Fennwald,S., Zendeui,J.G., Ojwang,J.O., Hogan,M.E.,
Pommier,Y. and Mazumder,A.
TITLE Guanosine-rich oligonucleotide integrase inhibitors
JOURNAL Patent: US 6355785-A 62 12-MAR-2002;
FEATURES Location/Qualifiers
1..17
source

BASE COUNT 0 a 0 c 12 g 5 t
ORIGIN

Query Match 91.7%; Score 11; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGG 11
|||||
Db 6 GGGGTGGTGGG 16

RESULT 8
ACCESSION AR200307
LOCUS Sequence 64 from patent US 6355785.
DEFINITION AR200307 linear PAT 20-APR-2002
ACCESSION AR200307
VERSION AR200307.1 GI:20250381
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Rando,R.F., Fennwald,S., Zendeui,J.G., Ojwang,J.O., Hogan,M.E.,
Pommier,Y. and Mazumder,A.
TITLE Guanosine-rich oligonucleotide integrase inhibitors
JOURNAL Patent: US 6355785-A 64 12-MAR-2002;
FEATURES Location/Qualifiers
1..17
source /organism="unknown"

BASE COUNT 0 a 0 c 12 g 5 t
ORIGIN

Query Match 91.7%; Score 11; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGGTGGTGGG 12
|||||
Db 3 GGGGTGGTGGG 13

RESULT 9
ACCESSION AR200308
LOCUS Sequence 65 from patent US 6355785.
DEFINITION AR200308 linear PAT 20-APR-2002
ACCESSION AR200308
VERSION AR200308.1 GI:20250382
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Rando,R.F., Fennwald,S., Zendeui,J.G., Ojwang,J.O., Hogan,M.E.,
Pommier,Y. and Mazumder,A.
TITLE Guanosine-rich oligonucleotide integrase inhibitors
JOURNAL Patent: US 6355785-A 65 12-MAR-2002;
FEATURES Location/Qualifiers
1..17
source /organism="unknown"

BASE COUNT 0 a 0 c 12 g 4 t 1 others
ORIGIN

Query Match 91.7%; Score 11; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGG 11
|||||
Db 6 GGGGTGGTGGG 16

RESULT 10
ACCESSION AR262436
LOCUS Sequence 62 from patent US 6323185.
DEFINITION AR262436 linear PAT 29-JAN-2003
ACCESSION AR262436
VERSION AR262436.1 GI:28073867
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Rando,R.F., Fennwald,S., Zendeui,J.G., Ojwang,J.O. and Hogan,M.E.
TITLE Anti-viral guanosine-rich oligonucleotides and method of treating
HIV
JOURNAL Patent: US 6323185-A 62 27-NOV-2001;
FEATURES Location/Qualifiers
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source /organism="unknown"

BASE COUNT 0 a 0 c 12 g 5 t
ORIGIN

Query Match 91.7%; Score 11; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGG 11
|||||
Db 6 GGGGTGGTGGG 16

RESULT 11

AR262438
 LOCUS AR262438 17 bp DNA linear PAT 29-JAN-2003
 DEFINITION Sequence 64 from patent US 6323185.
 ACCESSION AR262438
 VERSION AR262438.1 GI:28073869
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Rando,R.F., Fennwald,S., Zendeui,J.G., Ojwang,J.O. and Hogan,M.B.
 TITLE Anti-viral guanosine-rich oligonucleotides and method of treating HIV
 JOURNAL Patent: US 6323185-A 64 27-NOV-2001;
 FEATURES Location/Qualifiers
 source 1..17
 BASE COUNT 0 a 0 c 12 g 5 t
 ORIGIN
 Query Match 91.7%; Score 11; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GGGTGGTGGG 12
 Db |||||
 3 GGGTGGTGGG 13
 RESULT 12
 AR262439
 LOCUS AR262439 17 bp DNA linear PAT 29-JAN-2003
 DEFINITION Sequence 65 from patent US 6323185.
 ACCESSION AR262439
 VERSION AR262439.1 GI:28073870
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Rando,R.F., Fennwald,S., Zendeui,J.G., Ojwang,J.O. and Hogan,M.B.
 TITLE Anti-viral guanosine-rich oligonucleotides and method of treating HIV
 JOURNAL Patent: US 6323185-A 65 27-NOV-2001;
 FEATURES Location/Qualifiers
 source 1..17
 BASE COUNT 0 a 0 c 12 g 4 t 1 others
 ORIGIN
 Query Match 91.7%; Score 11; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGGGTGGTGGG 11
 Db |||||
 6 GGGGTGGTGGG 16
 RESULT 13
 AX284071
 LOCUS AX284071 17 bp DNA linear PAT 20-NOV-2001
 DEFINITION Sequence 36 from Patent WO0179487.
 ACCESSION AX284071
 VERSION AX284071.1 GI:17044781
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1
 AUTHORS Degitz,K.K. and Besch,R.
 TITLE Polydesoxyribonucleotides for inhibiting the expression of the icam-1-gene

JOURNAL Patent: WO 0179487-A 36 25-OCT-2001;
 FEATURES Degitz, Klaus Karl (DE); Besch, Robert (DE)
 source Location/Qualifiers
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 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 /note="Beschreibung der kunstlichen Sequenz:Polydesoxyribonukleotid"
 BASE COUNT 0 a 0 c 12 g 5 t
 ORIGIN
 Query Match 91.7%; Score 11; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGGGTGGTGGG 11
 Db |||||
 6 GGGGTGGTGGG 16
 RESULT 14
 AR078333
 LOCUS AR078333 20 bp DNA linear PAT 31-AUG-2000
 DEFINITION Sequence 2 from patent US 5962426.
 ACCESSION AR078333
 VERSION AR078333.1 GI:10005079
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Glazer,P.M.
 TITLE Triple-helix forming oligonucleotides for targeted mutagenesis
 JOURNAL Patent: US 5962426-A 2 05-OCT-1999;
 FEATURES Location/Qualifiers
 source 1..20
 BASE COUNT 3 a 0 c 15 g 2 t
 ORIGIN
 Query Match 91.7%; Score 11; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.4e+05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGGGTGGTGGG 11
 Db |||||
 10 GGGGTGGTGGG 20
 RESULT 15
 AR092032/c
 LOCUS AR092032 20 bp DNA linear PAT 08-SEP-2000
 DEFINITION Sequence 56 from patent US 5998141.
 ACCESSION AR092032
 VERSION AR092032.1 GI:10018786
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Acton,S.Laurence.
 TITLE Intronic and polymorphic SR-BI nucleic acids and uses therefor
 JOURNAL Patent: US 5998141-A 56 07-DEC-1999;
 FEATURES Location/Qualifiers
 source 1..20
 BASE COUNT 4 a 13 c 1 g 2 t
 ORIGIN
 Query Match 91.7%; Score 11; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.4e+05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGG 11
Db 13 GGGGTGGTGG 3

Search completed: October 27, 2003, 11:09:28
Job time : 251.743 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:29 ; Search time 108 Seconds

(without alignments)
299.938 Million cell updates/sec

Title: US-09-331-204A-13

Perfect score: 12

Sequence: 1 999999999999 12

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 1543890

Minimum DB seq length: 0

Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /SID1/gcgdata/geneseq/geneseq-nb1/NA1982.DAT.*
4: /SID1/gcgdata/geneseq/geneseq-nb1/NA1983.DAT.*
5: /SID1/gcgdata/geneseq/geneseq-nb1/NA1984.DAT.*
6: /SID1/gcgdata/geneseq/geneseq-nb1/NA1985.DAT.*
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13: /SID1/gcgdata/geneseq/geneseq-nb1/NA1992.DAT.*
14: /SID1/gcgdata/geneseq/geneseq-nb1/NA1993.DAT.*
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18: /SID1/gcgdata/geneseq/geneseq-nb1/NA1997.DAT.*
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23: /SID1/gcgdata/geneseq/geneseq-nb1/NA2001B.DAT.*
24: /SID1/gcgdata/geneseq/geneseq-nb1/NA2002.DAT.*
25: /SID1/gcgdata/geneseq/geneseq-nb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12	100.0	12	17	AA36248
2	12	100.0	12	20	AA36248
3	12	100.0	15	24	ABL39459
4	12	100.0	18	27	AA36196
5	12	100.0	18	20	AA360328
6	12	100.0	18	20	AA360332
7	12	100.0	18	20	AA360297
8	12	100.0	18	20	AA360290

Result No.	Score	Query Match	Length	ID	Description
9	12	100.0	18	21	AA299625
10	12	100.0	18	21	AA299650
11	12	100.0	21	17	AA36197
12	12	100.0	21	20	AA360329
13	12	100.0	21	20	AA360291
14	12	100.0	21	20	AA360291
15	12	100.0	21	20	AA360291
16	12	100.0	21	20	AA360291
17	12	100.0	21	20	AA360291
18	12	100.0	21	20	AA360291
19	12	100.0	21	20	AA360291
20	12	100.0	21	20	AA360291
21	12	100.0	21	20	AA360291
22	12	100.0	21	20	AA360291
23	12	100.0	21	20	AA360291
24	12	100.0	21	20	AA360291
25	12	100.0	21	20	AA360291
26	12	100.0	21	20	AA360291
27	12	100.0	21	20	AA360291
28	12	100.0	21	20	AA360291
29	12	100.0	21	20	AA360291
30	12	100.0	21	20	AA360291
31	12	100.0	21	20	AA360291
32	12	100.0	21	20	AA360291
33	12	100.0	21	20	AA360291
34	12	100.0	21	20	AA360291
35	12	100.0	21	20	AA360291
36	12	100.0	21	20	AA360291
37	12	100.0	21	20	AA360291
38	12	100.0	21	20	AA360291
39	12	100.0	21	20	AA360291
40	12	100.0	21	20	AA360291
41	12	100.0	21	20	AA360291
42	12	100.0	21	20	AA360291
43	12	100.0	21	20	AA360291
44	12	100.0	21	20	AA360291
45	12	100.0	21	20	AA360291

ALIGNMENTS

RESULT 1
AA36248
ID AAT36248 standard; DNA; 12 BP.

XX AAT36248;
XX AC
XX AAT36248;
DT 25-MAR-2003 (updated)
DT 16-APR-1997 (first entry)
XX
XX CD28 expression inhibiting oligonucleotide, RT18s.
XX DE
XX Reduction; T cell; CD28; gene expression; treatment; immune system;
KW disorder; graft versus host disease; septic shock; viral disease;
KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoidosis;
KW multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2;
KW systemic lupus erythematosus; inflammatory bowel disease;
KW IL-2; production; antisense; inhibition; ss
XX
XX Synthetic.
XX
XX WO9624380-A1.
XX
XX 15-AUG-1996.
XX
XX 05-FEB-1996;
XX 96WO-US01507.
XX
XX 09-FEB-1995;
XX 95US-0387041.
XX 18-SEP-1995;
XX 95US-0528878.
XX 09-FEB-1995;
XX 95US-0387041.
XX 18-SEP-1995;
XX 95US-0528878.

Nucleotide sequenc
Nucleotide sequenc
Triplex forming ol
CD28 inhibiting ph
CD28 inhibiting ol
Human ETEB allele-
Oligonucleotide pr
Oligonucleotide pr
Oligonucleotide SE
Oligonucleotide SE
Oligonucleotide SE
Oligonucleotide SE
Oligonucleotide SE
Viral integrase in
Viral integrase in
Viral integrase in
Oligonucleotide #5
Oligonucleotide #5
Oligonucleotide #5
ICAM-1 triple heli
Transcriptional ac
Cryptosporidium pa
Sequence of B-13-
supF gene triplex
Triplex-forming ol
Oligonucleotide AG
Human SR-BI gene e
Human SR-BI gene e
Murine SACI gene s
Guanosine rich oli
Viral integrase in
Oligonucleotide #1
Cryptosporidium pa
Triplex forming ol
Probe for characte
Oligonucleotide pr

PA (ICNC) ICN PHARM INC.
 XX Tam RC;
 XX WPI; 1996-384228/38.
 XX
 PT Oligo:nucleotide which reduces CD28 gene expression in T cells -
 PT for treating immune system diseases, e.g. graft vs. host disease,
 PT septic shock, psoriasis, etc.
 XX
 XX Example 2; Page 45; 77pp; English.
 XX
 CC The present oligonucleotide reduces CD28 dependent interleukin-2
 CC (IL-2) production and T cell CD28 gene expression, useful in the
 CC treatment of CD28 mediated diseases, particularly immune system
 CC disorders, e.g. graft versus host disease, septic shock, viral
 CC disease, psoriasis, type I diabetes mellitus, thyroiditis,
 CC sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis,
 CC systemic lupus erythematosus, inflammatory bowel disease, etc..
 CC Reducing CD28 expression may reduce the effects of antigenic
 CC stimulation of CD28 positive T cells, with a consequent reduction
 CC in cytokine release.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX
 XX Sequence 12 BP; 0 A; 0 C; 10 G; 2 T; 0 other;
 SQ
 Query Match 100.0%; Score 12; DB 17; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGGGTGGTGGG 12
 DB 1 GGGGTGGTGGG 12
 RESULT 2
 AAX90341
 ID AAX90341 standard; DNA; 12 BP.
 AC AAX90341;
 XX
 XX 24-SEP-1999 (first entry)
 DT
 XX
 DE CD28 inhibiting phosphorothioate oligonucleotide RT18S.
 XX
 XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
 KW immune system mediated disease; gamma-interferon; IL-8;
 KW phosphorothioate; ss.
 KW
 XX Synthetic.
 OS
 XX US5932556-A.
 PN
 XX 03-AUG-1999.
 XX
 XX 18-SEP-1995; 95US-0529878.
 PF
 XX
 XX 18-SEP-1995; 95US-0529878.
 PR
 XX (TAMR/) TAM R C.
 PA
 XX Tam RC;
 XX WPI; 1999-443609/37.
 XX
 XX Treatment of immune system-mediated diseases by inhibiting
 PT expression of CD28, IL-2, gamma-interferon or IL-8
 PT
 XX Example; Column 24; 45pp; English.
 PS
 XX The present invention describes a method for inhibiting the expression
 CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
 CC comprises simultaneous administration of an oligonucleotide (OGN).

CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
 CC method. The OGNs are used for the treatment of immune system-mediated
 CC diseases. The present sequence represents a CD28 inhibiting
 CC phosphorothioate oligonucleotide used in the exemplification of the
 CC present invention.
 XX
 SQ Sequence 12 BP; 0 A; 0 C; 10 G; 2 T; 0 other;
 Query Match 100.0%; Score 12; DB 20; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGGGTGGTGGG 12
 DB 1 GGGGTGGTGGG 12
 RESULT 3
 ABL39459
 ID ABL39459 standard; DNA; 15 BP.
 XX
 AC ABL39459;
 XX
 XX 22-APR-2002 (first entry)
 DT
 XX
 DE Human ETRF allele-specific oligonucleotide primer 19.
 XX
 XX Human; electron-transfer flavoprotein beta polypeptide; ETRF;
 KW electron acceptor; mitochondrial matrix; glutaric acidemia type II;
 KW novel polymorphic site; novel polymorphism; ETRF genotype; ss; GAI1;
 KW ETRF haplotype; transgenic animal; primer; probe; chromosome 19q13;
 KW primer-extension oligonucleotide; single nucleotide polymorphism;
 KW SNP.
 KW
 XX Homo sapiens.
 OS
 XX WO200202580-A2.
 FN
 XX 10-JAN-2002.
 PD
 XX 05-JUL-2001; 2001WO-US21306.
 PF
 XX 05-JUL-2000; 2000US-215984P.
 PR
 XX (GENA-) GENAISANCE PHARM INC.
 PA
 XX Bentivegna SC, Bieglecki KM, Kazemi A, Koshy B;
 PI
 XX WPI; 2002-154722/20.
 DR
 XX Novel isolated human electron-transfer-flavoprotein, beta
 PT polynucleotide, useful for therapeutic purposes, for studying the
 PT expression and function of the polynucleotide, and for expressing the
 PT flavoprotein
 XX
 PS Claim 17; Page 14; 143pp; English.
 XX
 CC The invention comprises DNA, cDNA and protein sequences of the human
 CC electron-transfer flavoprotein, beta polypeptide (ETRF) gene (located on
 CC chromosome 19q13.3-13.4). The invention specifically relates to the
 CC identification of 27 novel polymorphic sites within the ETRF gene.
 CC Electron-transfer flavoprotein (ETRF) is an obligatory electron acceptor
 CC for nine primary flavoprotein dehydrogenases and is located in the
 CC mitochondrial matrix. ETRF is composed of an alpha (ETFA) and a beta
 CC (ETFB) subunit. Electrons accepted by ETRF are transferred to the
 CC mitochondrial respiratory chain by ETRF dehydrogenases (ETRDHs).
 CC Deficiency of ETRF or ETRFDH leads to glutaric acidemia type II (GAI1).
 CC Therefore ETRF is a pharmaceutically-important gene in the treatment of
 CC GAI1. The novel ETRF polymorphisms identified in the invention are useful
 CC for genotyping and haplotyping the ETRF gene of an individual. The ETRF
 CC protein and nucleic acids of the invention are useful for studying the
 CC expression and function of ETRF in vivo. The ETRF protein and nucleic
 CC acids are also useful for testing the efficacy of therapeutic agents and

CC compounds for glutaric acidemia type II. The nucleic acids of the
CC invention are useful in the production of a transgenic animal expressing
CC the E7F8 gene. Nucleic acids ABL39414-ABL39440 represent claimed E7F8
CC allele-specific probes. Nucleic acids ABL39441-ABL39494 represent
CC claimed E7F8 allele-specific PCR primers. Nucleic acids ABL39495-ABL39548
CC represent claimed E7F8 primer-extension pligonucleotides.
XX
SQ Sequence 15 BP; 0 A; 0 C; 11 G; 3 T; 1 other;

Query Match 100.0%; Score 12; DB 24; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGGG 12
| | | | |
Db 2 GGGGTGGTGGGG 13

RESULT 4
AAT36196
ID AAT36196 standard; DNA; 18 BP.

XX AAT36196;
AC
DT 25-MAR-2003 (updated)
DT 15-APR-1997 (first entry)
XX
DE

Triplex forming oligo targetting CD28 5'-UTR (nt 58-75).

XX Reduction; T cell; CD28; gene expression; treatment; immune system;
XX disorder; graft versus host disease; septic shock; viral disease;
KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;
KW multiple sclerosis; uveitis; rheumatoid arthritis; 5'-UTR;
KW systemic lupus erythematosus; inflammatory bowel disease;
KW triplex forming; oligonucleotide; 5'-untranslated region; ss
XX
OS Synthetic.

XX WO9624380-A1.

XX PD 15-AUG-1996.

XX PF 05-FEB-1996; 96WO-US01507.

XX PR 09-FEB-1995; 95US-0387041.

XX PR 18-SEP-1995; 95US-0529878.

XX PR 09-FEB-1995; 95US-0387041.

XX PR 18-SEP-1995; 95US-0529878.

XX PA (ICNC) ICN PHARM INC.

XX PI Tam RC;

XX DR WPI; 1996-384228/38.

XX Oligo:nucleotide which reduces CD28 gene expression in T cells -
PT for treating immune system diseases, e.g. graft vs. host disease,
PT septic shock, psoriasis, etc.

XX Claim 9; Page 54; 77pp; English.

XX The present oligonucleotide reduces T cell CD28 gene expression,
CC useful in the treatment of CD28 mediated diseases, particularly
CC immune system disorders, e.g. graft versus host disease, septic
CC shock, viral disease, psoriasis, type I diabetes mellitus,
CC thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid
CC arthritis, systemic lupus erythematosus, inflammatory bowel
CC disease, etc.. Reducing CD28 expression may reduce the effects of
CC antigenic stimulation of CD28 positive T cells, with a consequent
CC reduction in cytokine release.
CC (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;

Query Match 100.0%; Score 12; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGGG 12
| | | | |
Db 7 GGGGTGGTGGGG 18

RESULT 5
AAX90328
ID AAX90328 standard; DNA; 18 BP.

XX AAX90328;
AC
DT 24-SEP-1999 (first entry)
XX
DE

CD28 inhibiting phosphorothioate oligonucleotide RT039.

XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
KW immune system mediated disease; gamma-interferon; IL-8;
KW phosphorothioate; ss.

XX Synthetic.

XX OS US5932556-A.

XX PN 03-AUG-1999.

XX PD 18-SEP-1995; 95US-0529878.

XX PR 18-SEP-1995; 95US-0529878.

XX (TAMR/) TAM R C.

XX PI Tam RC;

XX DR WPI; 1999-443609/37.

XX Treatment of immune system-mediated diseases by inhibiting
PT expression of CD28, IL-2, gamma-interferon or IL-8
XX Example; Column 21; 45pp; English.

XX The present invention describes a method for inhibiting the expression
CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
CC comprises subcutaneous administration of an oligonucleotide (OGN).
CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
CC method. The OGNs are used for the treatment of immune system-mediated
CC diseases. The present sequence represents a CD28 inhibiting
CC phosphorothioate oligonucleotide used in the exemplification of the
CC present invention.

XX Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;

Query Match 100.0%; Score 12; DB 20; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGGG 12
| | | | |
Db 7 GGGGTGGTGGGG 18

RESULT 6
AAX90332/c

ID AAX90332 standard; DNA; 18 BP.

XX AAX90332;
AC
DT 24-SEP-1999 (first entry)
XX

DE CD28 inhibiting phosphorothioate oligonucleotide RTC06S.
XX
KW CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
KW immune system mediated disease; gamma-interferon; IL-8;
KW phosphorothioate; ss.
XX
OS Synthetic.
XX
XX US5932556-A.
XX
PD 03-AUG-1999.
XX
XX 18-SEP-1995; 95US-0529878.
XX
XX 18-SEP-1995; 95US-0529878.
XX
PA (TAMR/) TAM R C.
XX
XX Tam RC;
XX
DR WPI; 1999-443609/37.
XX
XX Treatment of immune system-mediated diseases by inhibiting
PT expression of CD28, IL-2, gamma-interferon or IL-8
XX
XX Example; Column 21; 45pp; English.
XX
CC The present invention describes a method for inhibiting the expression
CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
CC comprises subcutaneous administration of an oligonucleotide (OGN).
CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
CC method. The OGNs are used for the treatment of immune system-mediated
CC diseases. The present sequence represents a CD28 inhibiting
CC phosphorothioate oligonucleotide used in the exemplification of the
CC present invention.
XX
SQ Sequence 18 BP; 4 A; 13 C; 0 G; 1 T; 0 other;
XX
XX Query Match 100.0%; Score 12; DB 20; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 9.9e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 GGGGTGGTGGG 12
DB 18 GGGGTGGTGGG 7
XX
RESULT 7
AAX90297/c
ID AAX90297 standard; DNA; 18 BP.
XX
AC AAX90297;
XX
XX 24-SEP-1999 (first entry)
XX
XX Oligonucleotide RTC06 used in an Example from US5932556.
DE
XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
XX immune system mediated disease; gamma-interferon; IL-8; ss.
XX
XX Synthetic.
XX
XX US5932556-A.
XX
XX 03-AUG-1999.
XX
XX 18-SEP-1995; 95US-0529878.
XX
XX 18-SEP-1995; 95US-0529878.
XX
XX 18-SEP-1995; 95US-0529878.
XX
XX (TAMR/) TAM R C.
XX
XX Tam RC;
XX
PI

DE CD28 inhibiting phosphorothioate oligonucleotide RTC06S.
XX
KW CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
KW immune system mediated disease; gamma-interferon; IL-8;
KW phosphorothioate; ss.
XX
OS Synthetic.
XX
XX US5932556-A.
XX
PD 03-AUG-1999.
XX
XX 18-SEP-1995; 95US-0529878.
XX
XX 18-SEP-1995; 95US-0529878.
XX
PA (TAMR/) TAM R C.
XX
XX Tam RC;
XX
DR WPI; 1999-443609/37.
XX
XX Treatment of immune system-mediated diseases by inhibiting
PT expression of CD28, IL-2, gamma-interferon or IL-8
XX
XX Example; Column 21; 45pp; English.
XX
CC The present invention describes a method for inhibiting the expression
CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
CC comprises subcutaneous administration of an oligonucleotide (OGN).
CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
CC method. The OGNs are used for the treatment of immune system-mediated
CC diseases. The present sequence represents a CD28 inhibiting
CC phosphorothioate oligonucleotide used in the exemplification of the
CC present invention.
XX
SQ Sequence 18 BP; 4 A; 13 C; 0 G; 1 T; 0 other;
XX
XX Query Match 100.0%; Score 12; DB 20; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 9.9e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 GGGGTGGTGGG 12
DB 18 GGGGTGGTGGG 7
XX
RESULT 7
AAX90297/c
ID AAX90297 standard; DNA; 18 BP.
XX
AC AAX90297;
XX
XX 24-SEP-1999 (first entry)
XX
XX Oligonucleotide RTC06 used in an Example from US5932556.
DE
XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
XX immune system mediated disease; gamma-interferon; IL-8; ss.
XX
XX Synthetic.
XX
XX US5932556-A.
XX
XX 03-AUG-1999.
XX
XX 18-SEP-1995; 95US-0529878.
XX
XX 18-SEP-1995; 95US-0529878.
XX
XX (TAMR/) TAM R C.
XX
XX Tam RC;
XX
PI

XX WPI; 1999-443609/37.
XX
XX Treatment of immune system-mediated diseases by inhibiting
PT expression of CD28, IL-2, gamma-interferon or IL-8
XX
XX Example; Column 13; 45pp; English.
XX
XX The present invention describes a method for inhibiting the expression
CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
CC comprises subcutaneous administration of an oligonucleotide (OGN).
CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
CC method. The OGNs are used for the treatment of immune system-mediated
CC diseases. AAX90292 to AAX90323 represent oligonucleotides used in the
CC exemplification of the present invention.
XX
XX Sequence 18 BP; 4 A; 13 C; 0 G; 1 T; 0 other;
XX
XX Query Match 100.0%; Score 12; DB 20; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 9.9e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 GGGGTGGTGGG 12
DB 18 GGGGTGGTGGG 7
XX
RESULT 8
AAX90290
ID AAX90290 standard; DNA; 18 BP.
XX
AC AAX90290;
XX
XX 24-SEP-1999 (first entry)
XX
XX CD28 inhibition oligonucleotide RT03.
XX
XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
XX immune system mediated disease; gamma-interferon; IL-8; ss.
XX
XX Synthetic.
XX
XX US5932556-A.
XX
XX 03-AUG-1999.
XX
XX 18-SEP-1995; 95US-0529878.
XX
XX 18-SEP-1995; 95US-0529878.
XX
XX (TAMR/) TAM R C.
XX
XX Tam RC;
XX
XX WPI; 1999-443609/37.
XX
XX Treatment of immune system-mediated diseases by inhibiting
PT expression of CD28, IL-2, gamma-interferon or IL-8
XX
XX Claim 5; Column 29; 45pp; English.
XX
XX The present invention describes a method for inhibiting the expression
CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
CC comprises subcutaneous administration of an oligonucleotide (OGN).
CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
CC method. The OGNs are used for the treatment of immune system-mediated
CC diseases.
XX
XX Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;
XX
XX Query Match 100.0%; Score 12; DB 20; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 9.9e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
PI

QY 1 GGGGTGGTGGG 12
 |||||
 Db 7 GGGGTGGTGGG 18

RESULT 9
 AAZ99625
 ID AAZ99625 standard; DNA; 18 BP.
 XX
 AC AAZ99625;
 XX
 DT 12-JUL-2000 (first entry)
 XX

DE Nucleotide sequence of G-motif oligonucleotide GRI.

XX G-motif oligonucleotide; vaccine; Toxoplasmosis; viral infection;
 KW antigen presenting cell activation; natural killer cell; septic shock;
 KW cytotoxic T-lymphocyte; inflammation; autoimmune disease;
 KW rheumatoid arthritis; Crohn's disease; sarcoidosis; multiple sclerosis;
 KW Kawasaki syndrome; graft-versus-host disease; transplant rejection;
 KW helper T cell response 1-mediated disease; Lyme arthritis;
 KW Streptococcal induced arthritis; chronic inflammatory bowel disease;
 KW psoriasis vulgaris; experimental allergic encephalomyelitis;
 KW insulin-dependent diabetes mellitus; bacterial infection;
 KW parasitic infection; Leishmaniasis; spontaneous abortion; tumour; ss.
 XX

OS Synthetic.

XX WO200014217-A2.

XX 16-MAR-2000.

PD 03-SEP-1999; 99WO-EP06502.

PF 03-SEP-1998; 98EP-0116652.

PR (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.

XX Wagner H, Lipford GB, Heeg K;
 XX WPI; 2000-256970/22.

XX Compositions comprising G-motif oligonucleotides useful for treating
 PT e.g. septic shock, rheumatoid arthritis, diabetes and human
 PT immunodeficiency virus infections -
 XX Example 14; Page 32; 75pp; English.

XX The present sequence represents a G-motif oligonucleotide of the
 CC invention. The specification describes compositions comprising G-motif
 CC oligonucleotides. The G-motif oligonucleotides inhibit activation of
 CC antigen presenting cells by inhibiting the uptake of DNA by a cell, by
 CC stimulating natural killer cells, or by co-stimulating cytotoxic
 CC T-lymphocytes. The G-motif oligonucleotides may be used for the
 CC production of vaccines for treating septic shock, inflammation,
 CC autoimmune diseases (e.g. rheumatoid arthritis, Crohn's disease,
 CC sarcoidosis, multiple sclerosis, Kawasaki syndrome, graft-versus-host
 CC disease and transplant rejection), helper T cell response 1-mediated
 CC diseases (e.g. Streptococcal induced arthritis, Lyme arthritis, chronic
 CC inflammatory bowel disease, psoriasis vulgaris, experimental allergic
 CC encephalomyelitis, and insulin-dependent diabetes mellitus), bacterial
 CC infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis),
 CC viral infections (e.g. Cytomegalovirus and human immunodeficiency virus
 CC (HIV)-infections), spontaneous abortions and tumours. They may also be
 CC used to induce proliferation of bone marrow cells, especially macrophage
 CC precursor cells.

XX Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;

Query Match 100.0%; Score 12; DB 21; Length 18;
 Best Local Similarity 100.0%; Pred. No. 9.9e-03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 12
 |||||
 Db 7 GGGGTGGTGGG 18

RESULT 10
 AAZ99650/C
 ID AAZ99650 standard; DNA; 18 BP.
 XX
 AC AAZ99650;
 XX
 DT 12-JUL-2000 (first entry)
 XX

DE Nucleotide sequence of non-G-motif oligonucleotide GRFicomp.

XX G-motif oligonucleotide; vaccine; Toxoplasmosis; viral infection;
 KW antigen presenting cell activation; natural killer cell; septic shock;
 KW cytotoxic T-lymphocyte; inflammation; autoimmune disease;
 KW rheumatoid arthritis; Crohn's disease; sarcoidosis; multiple sclerosis;
 KW Kawasaki syndrome; graft-versus-host disease; transplant rejection;
 KW helper T cell response 1-mediated disease; Lyme arthritis;
 KW Streptococcal induced arthritis; chronic inflammatory bowel disease;
 KW psoriasis vulgaris; experimental allergic encephalomyelitis;
 KW insulin-dependent diabetes mellitus; bacterial infection;
 KW parasitic infection; Leishmaniasis; spontaneous abortion; tumour; ss.
 XX

OS Synthetic.

XX WO200014217-A2.

XX 16-MAR-2000.

PD 03-SEP-1999; 99WO-EP06502.

PF 03-SEP-1998; 98EP-0116652.

PR (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.

XX Wagner H, Lipford GB, Heeg K;
 XX WPI; 2000-256970/22.

XX Compositions comprising G-motif oligonucleotides useful for treating
 PT e.g. septic shock, rheumatoid arthritis, diabetes and human
 PT immunodeficiency virus infections -
 XX Example 14; Page 32; 75pp; English.

XX The present sequence represents a non-G-motif oligonucleotide of the
 CC invention. The specification describes compositions comprising G-motif
 CC oligonucleotides. The G-motif oligonucleotides inhibit activation of
 CC antigen presenting cells by inhibiting the uptake of DNA by a cell, by
 CC stimulating natural killer cells, or by co-stimulating cytotoxic
 CC T-lymphocytes. The G-motif oligonucleotides may be used for the
 CC production of vaccines for treating septic shock, inflammation,
 CC autoimmune diseases (e.g. rheumatoid arthritis, Crohn's disease,
 CC sarcoidosis, multiple sclerosis, Kawasaki syndrome, graft-versus-host
 CC disease and transplant rejection), helper T cell response 1-mediated
 CC diseases (e.g. Streptococcal induced arthritis, Lyme arthritis, chronic
 CC inflammatory bowel disease, psoriasis vulgaris, experimental allergic
 CC encephalomyelitis, and insulin-dependent diabetes mellitus), bacterial
 CC infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis),
 CC viral infections (e.g. Cytomegalovirus and human immunodeficiency virus
 CC (HIV)-infections), spontaneous abortions and tumours. They may also be
 CC used to induce proliferation of bone marrow cells, especially macrophage
 CC precursor cells.

XX Sequence 18 BP; 4 A; 13 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 12; DB 21; Length 18;
 Best Local Similarity 100.0%; Pred. No. 9.9e-03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGG 12
Db 12 GGGGTGGTGGG 1

RESULT 11

AAT36197

ID AAT36197 standard; DNA; 21 BP.

XX

AC AAT36197;

XX

DT 25-MAR-2003 (updated)

XX

DT 15-APR-1997 (first entry)

XX

DE Triplex forming oligo targeting CD28 5'-UTR (nt 58-78).

XX

KW Reduction; T cell; CD28; gene expression; treatment; immune system;

XX

KW disorder; graft versus host disease; septic shock; viral disease;

XX

KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;

XX

KW multiple sclerosis; uveitis; rheumatoid arthritis; 5'-UTR;

XX

KW systemic lupus erythematosus; inflammatory bowel disease;

XX

KW triplex forming; oligonucleotide; 5'-untranslated region; ss

XX

OS Synthetic.

XX

PN WO9624380-A1.

XX

PD 15-AUG-1996.

XX

PF 05-FEB-1996; 96WO-US01507.

XX

PR 09-FEB-1995; 95US-0387041.

XX

PR 18-SEP-1995; 95US-0529878.

XX

PR 09-FEB-1995; 95US-0387041.

XX

PR 18-SEP-1995; 95US-0529878.

XX

PA (ICNC) ICN PHARM INC.

XX

PI Tam RC;

XX

XX WPI; 1996-384228/38.

DR

XX

XX Oligo:nucleotide which reduces CD28 gene expression in T cells

PT

PT for treating immune system diseases, e.g. graft vs. host disease,

PT

PT septic shock, psoriasis, etc.

XX

PS Claim 10; Page 54; 77pp; English.

XX

XX The present oligonucleotide reduces T cell CD28 gene expression,

CC

CC useful in the treatment of CD28 mediated diseases, particularly

CC

CC immune system disorders, e.g. graft versus host disease, septic

CC

CC shock, viral disease, psoriasis, type I diabetes mellitus,

CC

CC thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid

CC

CC arthritis, systemic lupus erythematosus, inflammatory bowel

CC

CC disease, etc.. Reducing CD28 expression may reduce the effects of

CC

CC antigenic stimulation of CD28 positive T cells, with a consequent

CC

CC reduction in cytokine release.

XX

XX (Updated on 25-MAR-2003 to correct PR field.)

XX

XX Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;

ID AAX90329 standard; DNA; 21 BP.

XX

AC AAX90329;

XX

DT 24-SEP-1999 (first entry)

XX

DE

XX

XX CD28 inhibiting phosphorothioate oligonucleotide RT04S.

XX

KW CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;

KW

KW immune system mediated disease; gamma-interferon; IL-8;

XX

XX phosphorothioate; ss.

XX

OS Synthetic.

XX

XX US5932556-A.

PN

XX

PD 03-AUG-1999.

XX

PF 18-SEP-1995; 95US-0529878.

XX

PR 18-SEP-1995; 95US-0529878.

XX

XX (TAMR/) TAM R C.

PA

XX

PI Tam RC;

XX

XX WPI; 1999-443609/37.

DR

XX

XX Treatment of immune system-mediated diseases by inhibiting

PT

PT expression of CD28, IL-2, gamma-interferon or IL-8

XX

XX Example; Column 21; 45pp; English.

PS

XX

XX The present invention describes a method for inhibiting the expression

CC

CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method

CC

CC comprises subcutaneous administration of an oligonucleotide (OGN).

CC

CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the

CC

CC method. The OGNs are used for the treatment of immune system-mediated

CC

CC diseases. The present sequence represents a CD28 inhibiting

CC

CC phosphorothioate oligonucleotide used in the exemplification of the

CC

XX present invention.

XX

SQ Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;

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XX PR 18-SEP-1995; 95US-0529878.
XX PA (TAMR/) TAM R C.
XX PI Tam RC;
XX XX WPI; 1999-443609/37.
XX DR Treatment of immune system-mediated diseases by inhibiting
XX PT expression of CD28, IL-2, gamma-interferon or IL-8
XX PT Claim 6; Column 29; 45pp; English.
XX PS
XX CC The present invention describes a method for inhibiting the expression
XX CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
XX CC comprises subcutaneous administration of an oligonucleotide (OGN).
XX CC AAX90298 to AAX90291 represent specifically claimed OGNs for use in the
XX CC method. The OGNs are used for the treatment of immune system-mediated
XX CC diseases.
XX CC
XX SQ Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;
XX
XX Query Match 100.0%; Score 12; DB 20; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 9.8e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GGGGTGGTGGGG 12
XX Db 10 GGGGTGGTGGGG 21
XX
XX RESULT 14
XX ABL39458/C
XX ID ABL39458 standard; DNA; 15 BP.
XX AC ABL39458;
XX
XX DT 22-APR-2002 (first entry)
XX DE Human ETPF allele-specific oligonucleotide primer 18.
XX
XX KW Human; electron-transfer flavoprotein beta polypeptide; ETPF;
XX KW electron acceptor; mitochondrial matrix; glutaric acidemia type II;
XX KW novel polymorphic site; novel polymorphism; ETPF genotype; ss; GAI;
XX KW ETPF haplotype; transgenic animal; primer; probe; chromosome 19q13;
XX KW primer-extension oligonucleotide; single nucleotide polymorphism;
XX KW SNP.
XX
XX OS Homo sapiens.
XX
XX PN WO200202580-A2.
XX
XX PD 10-JAN-2002.
XX
XX PF 05-JUL-2001; 2001WO-US21306.
XX
XX PR 05-JUL-2000; 2000US-215984P.
XX
XX PA (GENA-) GENAISSANCE PHARM INC.
XX
XX PI Bentivegna SC, Bieglecki KM, Kazemi A, Koshy B;
XX
XX DR WPI; 2002-154722/20.
XX
XX PT Novel isolated human electron-transfer-flavoprotein, beta
XX PT polynucleotide, useful for therapeutic purposes, for studying the
XX PT expression and function of the polynucleotide, and for expressing the
XX PT flavoprotein.
XX
XX PS Claim 17; Page 14; 143pp; English.
XX
XX CC The invention comprises DNA, cDNA and protein sequences of the human

```

```

XX CC electron-transfer flavoprotein, beta polypeptide (ETPF) gene (located on
XX CC chromosome 19q13.3-13.4). The invention specifically relates to the
XX CC identification of 27 novel polymorphic sites within the ETPF gene.
XX CC Electron-transfer flavoprotein (ETP) is an obligatory electron acceptor
XX CC for nine primary flavoprotein dehydrogenases and is located in the
XX CC mitochondrial matrix. ETP is composed of an alpha (ETPA) and a beta
XX CC (ETPB) subunit. Electrons accepted by ETP are transferred to the
XX CC mitochondrial respiratory chain by ETP dehydrogenases (ETPDHs).
XX CC Deficiency of ETP or ETPDH leads to glutaric acidemia type II (GAI).
XX CC Therefore ETPF is a pharmaceutically important gene in the treatment of
XX CC GAI. The novel ETPF polymorphisms identified in the invention are useful
XX CC for genotyping and haplotyping the ETPF gene of an individual. The ETPF
XX CC protein and nucleic acids of the invention are useful for studying the
XX CC expression and function of ETPF in vivo. The ETPF protein and nucleic
XX CC acids are also useful for testing the efficacy of therapeutic agents and
XX CC compounds for glutaric acidemia type II. The nucleic acids of the
XX CC invention are useful in the production of a transgenic animal expressing
XX CC the ETPF gene. Nucleic acids ABL39414-ABL39440 represent claimed ETPF
XX CC allele-specific probes. Nucleic acids ABL39441-ABL39494 represent
XX CC claimed ETPF allele-specific PCR primers. Nucleic acids ABL39495-ABL39548
XX CC represent claimed ETPF primer-extension oligonucleotides.
XX
XX SQ Sequence 15 BP; 3 A; 10 C; 1 G; 0 U; 1 other;
XX
XX Query Match 96.7%; Score 11.6; DB 24; Length 15;
XX Best Local Similarity 91.7%; Pred. No. 1.5e+04;
XX Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GGGGTGGTGGGG 12
XX Db 14 RGGGTGGTGGGG 3
XX
XX RESULT 15
XX ABH83464/C
XX ID ABH83464 standard; DNA; 12 BP.
XX
XX AC ABH83464;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 283457 for detecting SNP TSC0011318.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB00713.
XX
XX PR 07-APR-2000; 2000DE-1019173.
XX
XX PA (EPIC-) EPiGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single nucleotide polymorphisms and cytosine
XX PT methylation status.
XX
XX PS Claim 1; SEQ ID 283457; 29pp + Sequence Listing; German.
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

```

CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC AEC00010-AB099989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC AB100010-AB182073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX

SQ Sequence 12 BP; 2 A; 10 C; 0 G; 0 U; 0 other;

Query Match 91.7%; Score 11; DB 23; Length 12;

Best Local Similarity 100.0%; Pred. No. 2.9e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 11

Db 11 GGGGTGGTGGG 1

Search completed: October 27, 2003, 11:25:21

Job time : 108 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:29 ; Search time 1054.51 Seconds
(without alignments)
276.576 Million cell updates/sec

Title: US-09-331-204A-13

Perfect score: 12

Sequence: 1 9999tggc9999 12

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 11152

Minimum DB seq length: 0

Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpi:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	10.4	86.7	16	9	AI590540 twl1c02.x
C 2	10.4	86.7	19	9	AI807936 wf52e09.x
3	10.4	86.7	19	28	AZ369361 IM0119123
4	10.4	86.7	19	28	AZ381798 IM0138G01

C	5	10.4	86.7	19	28	AZ447936	AI590540
	6	10.4	86.7	19	28	AZ780591	twl1c02.x
	7	10.4	86.7	19	28	AZ786308	NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2259362 3', similar to TR:O00599 O00599 CON1.; mRNA sequence.
	8	10.4	86.7	20	28	AZ462338	AI590540
	9	10.4	86.7	21	28	AZ495585	EST.
	10	10.4	86.7	21	28	AZ774703	EST.
	11	10.4	86.7	22	9	AI183338	Homo sapiens (human)
	12	10.4	86.7	22	9	AI439277	Homo sapiens
	13	10.4	86.7	22	28	AZ766712	Homo sapiens
	14	10.4	86.7	22	28	AZ769521	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
	15	10	83.3	19	9	AA928040	1 (bases 1 to 16)
	16	10	83.3	21	28	AZ758704	NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
	17	10	83.3	22	9	AA923820	National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BRGAP), Tumor Gene Index
	18	10	83.3	22	9	AI354432	Unpublished
	19	9.4	78.3	16	9	AI569544	Contact: Robert Strausberg, Ph.D.
	20	9.4	78.3	16	9	AI684114	Email: cgapbs-r@mail.nih.gov
	21	9.4	78.3	16	9	AA909236	Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmart-Buck, M.D., Ph.D.
	22	9.4	78.3	19	9	AI1364573	CDNA Library Preparation: Life Technologies, Inc.
	23	9.4	78.3	21	28	AZ468862	CDNA Library Arrayed by: Greg Lennon, Ph.D.
	24	9.4	78.3	21	28	AZ512534	DNA Sequencing by: Washington University Genome Sequencing Center
	25	9.4	78.3	21	28	AZ783943	Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
	26	9.4	78.3	21	28	AZ788597	
	27	9.4	78.3	21	28	AZ864022	
	28	9.4	78.3	22	9	AI687266	
	29	9.4	78.3	22	9	AI1707945	
	30	9.4	78.3	22	13	BQ585098	
	31	9.4	78.3	22	28	AZ327083	
	32	9.4	78.3	22	28	AZ454940	
	33	9.4	78.3	22	28	AZ627938	
	34	9.4	78.3	22	28	AZ953028	
	35	9	75.0	20	14	D20001	
	36	9	75.0	21	28	AZ399828	
	37	8.8	73.3	12	13	BQ585390	
	38	8.8	73.3	13	13	BQ595080	
	39	8.8	73.3	14	13	BQ593114	
	40	8.8	73.3	15	13	BQ590018	
	41	8.8	73.3	16	9	AA937364	
	42	8.8	73.3	16	9	AA968729	
	43	8.8	73.3	16	9	AI209036	
	44	8.8	73.3	16	9	AI446372	
	45	8.8	73.3	16	9	AI648507	

ALIGNMENTS

RESULT 1
AI590540/C
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 353 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1
POLYA=No.

FEATURES

source

Location/Qualifiers
1..16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2359240"
/tissue_type="tumor, 5 pooled (see description)"
/lab_host="DH10B"
/clone_lib="NCI CGAP Brn52"
/note="Organ: Brain; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; This library represents the normalized
version of NCI CGAP Brn5. Cloned unidirectionally.
Primer: Oligo dT. Average insert size 1.19 kb. Tumor
types include: meningioma, oligodendroglioma, astrocytoma
(grade II), medulloblastoma, astrocytoma (grade IV).
Constructed by Life Technologies."

BASE COUNT
ORIGIN

4 a 12 c 0 g 0 t

Query Match 86.7%; Score 10.4; DB 9; Length 16;
Best Local Similarity 91.7%; Pred. No. 6.9e+05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGGG 12

Db 14 GTGGTGGTGGGG 3

RESULT 2

AI807936/c

LOCUS

DEFINITION w52e09.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone
IMAGE:2359240 3, similar to TR:Q39600 Q39600 EXTENSIN. ; contains
element MSR1 repetitive element ;, mRNA sequence.

ACCESSION

AI807936

VERSION

AI807936.1

GI:5394502

EST.

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 19)

NCI CGAP

http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgaps-rc@mail.nih.gov

This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Insert Length: 724 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1..19

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2359240"

/lab_host="DH10B"

/clone_lib="Soares NFL T GBC S1"

/note="Organ: Pooled; Vector: PT73D-Pac (Pharmacia) with

a modified polylinker; Site 1: Not I; Site 2: Eco RI;

Equal amounts of plasmid DNA from three normalized

libraries (fetal lung NBHL19W, testis NHT, and B-cell

NCI CGAP GCBI) were mixed, and ss circles were made in
vitr. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "

BASE COUNT
ORIGIN

3 a 16 c 0 g 0 t

Query Match 86.7%; Score 10.4; DB 9; Length 19;
Best Local Similarity 91.7%; Pred. No. 6.9e+05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGGG 12

Db 17 GGGGTGGTGGGG 6

RESULT 3

AZ369361

LOCUS

DEFINITION AZ369361 19 bp DNA linear GSS 02-OCT-2000
clone UUGC1M0119123 R, genomic survey sequence.

ACCESSION

AZ369361

VERSION

AZ369361.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Bescorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly,

M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhauser, A.

and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: gdunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0119 row: 1 column: 23

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1..19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0119123"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWP42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 0 c 18 g 1 t

ORIGIN

Query Match 86.7%; Score 10.4; DB 28; Length 19;
Best Local Similarity 91.7%; Pred. No. 6.9e+05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGGG 12

Db 2 GGGGTGGG 13

RESULT 4

AZ381798 19 bp DNA linear GSS 02-OCT-2000
LOCUS
DEFINITION
IM0138G01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0138G01 R, genomic survey sequence.

ACCESSION AZ381798

VERSION AZ381798.1 GI:10495498

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0138 row: G column: 01

Seq primer: CACACGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1..19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0138G01"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWP42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 0 c 15 g 4 t

ORIGIN

Query Match 86.7%; Score 10.4; DB 28; Length 19;

Best Local Similarity 91.7%; Pred. No. 6.9e+05;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGGG 12

Db 7 GTGGTGGTGGGG 18

RESULT 5

AZ447936/c

LOCUS

DEFINITION

IM0245O18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0245O18 F, genomic survey sequence.

ACCESSION AZ447936

VERSION AZ447936.1 GI:10600230

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0245 row: O column: 18

Seq primer: CTTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1..19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0245O18"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 1 a 18 c 0 g 0 t
ORIGIN
Query Match 86.7%; Score 10.4; DB 28; Length 19;
Best Local Similarity 91.7%; Pred. No. 6.9e+05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGGG 12
||| ||||| |||||
Db 18 GGGGTGGG GGG 7

RESULT 6
LOCUS A2780591 19 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0018B09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0018B09 F, genomic survey sequence.

ACCESSION A2780591
VERSION A2780591.1 GI:12912422
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
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Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0018 row: B column: 09
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source
1..19
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0018B09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male); was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 0 c 18 g 1 t
ORIGIN
Query Match 86.7%; Score 10.4; DB 28; Length 19;
Best Local Similarity 91.7%; Pred. No. 6.9e+05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGGG 12
||| ||||| |||||
Db 3 GGGGTGGG GGG 14

RESULT 7
LOCUS A2786308 19 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0031B17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0031B17 R, genomic survey sequence.

ACCESSION A2786308
VERSION A2786308.1 GI:12923936
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0031 row: B column: 17
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source
1..19
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0031B17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male); was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance." 1 t

BASE COUNT 2 a 1 c 15 g

ORIGIN

Query Match 86.7%; Score 10.4; DB 28; Length 19;

Best Local Similarity 91.7%; Pred. No. 6.9e+05; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGGG 12

Db 5 GGGGAGTGGGG 16

RESULT 8

AZ466238

LOCUS

DEFINITION IM0276J16R Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M0276J16 R, genomic survey sequence.

ACCESSION AZ466238

VERSION AZ466238.1

KEYWORDS GI:10624363

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

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Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0276 row: J column: 16

Seq primer: CACACAGGAAACAGTATGACC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

FEATURES

source

1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0276J16"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance." 4 a 0 c 12 g

BASE COUNT 4 a 0 c 12 g

ORIGIN

Query Match 86.7%; Score 10.4; DB 28; Length 20;

Best Local Similarity 91.7%; Pred. No. 6.9e+05;

Mismatches 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGGG 12

Db 5 GGGGTGGTGGGG 16

RESULT 9

AZ495585/c

LOCUS

DEFINITION IM0331H02R Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M0331H02 R, genomic survey sequence.

ACCESSION AZ495585

VERSION AZ495585.1

KEYWORDS GI:10671122

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0331 row: H column: 02

Seq primer: CACACAGGAAACAGTATGACC

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1..21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUC1M0331H02"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt ended and repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 2 a 1 g 2 t
ORIGIN

Query Match 86.7%; Score 10.4; DB 28; Length 21;
Best Local Similarity 91.7%; Pred. No. 6.9e+05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 12
|||||
Db 21 GGGGTGGG 10

RESULT 10
LOCUS AZ774703 21 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0004G14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0004G14 F, genomic survey sequence.

ACCESSION AZ774703
VERSION GSS.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plats: 0004 row: G column: 14
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0004G14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

FEATURES
source
1. .22
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1732030"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal heart NBH19W"
/notes="Organ: heart; Vector: p773D (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCATCTGAGTGGGCGGCGCATCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p773 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt ended and repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 2 a 19 c 0 g 0 t
ORIGIN

Query Match 86.7%; Score 10.4; DB 28; Length 21;
Best Local Similarity 91.7%; Pred. No. 6.9e+05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 12
|||||
Db 17 GGGGTGGG 6

RESULT 11
LOCUS A1183338/c 22 bp mRNA linear EST 28-OCT-1998
DEFINITION Q441a12.X1 Soares fetal heart NBH19W Homo sapiens cDNA clone IMAGE:1732030 3', similar to TR:Q18444 Q18444 COSMID C34D4.1, mRNA sequence.

ACCESSION A1183338
VERSION A1183338.1 GI:3733976
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 22)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 698 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1. .22
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1732030"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal heart NBH19W"
/notes="Organ: heart; Vector: p773D (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCATCTGAGTGGGCGGCGCATCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p773 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by

FEATURES
source
1. .22
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1732030"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal heart NBH19W"
/notes="Organ: heart; Vector: p773D (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCATCTGAGTGGGCGGCGCATCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p773 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by

M.Fatima Bernaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBHL19W."

BASE COUNT 4 a 16 c 0 g 2 t

ORIGIN

Query Match 86.7%; Score 10.4; DB 9; Length 22;
Best Local Similarity 91.7%; Pred. No. 7e+05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 12
Db 12 GGGGTGGTGGG 1

RESULT 12

AI439277/c

LOCUS

AI439277 22 bp mRNA linear EST 09-MAR-1999
ti34a02.x1 NCI CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2134250 3'
similar to TR:Q17089 Q17089 COLLAGEN ; contains element MER22
repetitive element ;, mRNA sequence.

ACCESSION

AI439277

VERSION

AI439277.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 22)

AUTHORS

NCI-CGAP

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Life Technologies catalog #: 11547-015
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Seq primer: -400P from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1..22

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2134250"

/tissue_type="lymphoma, follicular mixed small and large

cell"

/lab_host="DH10B"

/clone_lib="NCI-CGAP_Lym12"

/note="Organ: lymph node; Vector: pCMV-SPORT6; Site: 1;
Salt; Site: 2; NotI; Cloned unidirectionally. Primer:
Oligo dt. Average insert size 1.25 kb. Life Technologies
catalog #: 11547-015"

BASE COUNT 1 a 17 c 1 g 3 t

ORIGIN

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Best Local Similarity 91.7%; Pred. No. 7e+05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 12
Db 17 GGGGTGGTGGG 6

RESULT 13

AZ766712/c

LOCUS

AZ766712

22 bp DNA linear

GSS 16-FEB-2001

DEFINITION

IM056403R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0564A03 R, genomic survey sequence.

ACCESSION

AZ766712

VERSION

AZ766712.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 22)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
and Wright,D., Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished

JOURNAL

COMMENT

Contact: Robert B. Weiss

University of Utah Genomic Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0564 row: A column: 03

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1..22

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/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0564A03"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified Genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 1 a 21 c 0 g 0 t

ORIGIN

Query Match 86.7%; Score 10.4; DB 28; Length 22;

Best Local Similarity 91.7%; Pred. No. 7e+05;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 12

Db 21 GGGGTGGTGGG 10

RESULT 14

AZ769521/c

LOCUS AZ769521 22 bp DNA linear GSS 16-FEB-2001
 DEFINITION 1M0570018F Mouse 10kb plasmid TUGC1M library Mus musculus genomic
 clone UUGC1M0570018 F, genomic survey sequence.
 ACCESSION AZ769521
 VERSION AZ769521.1 GI:12889741
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 22)
 REFERENCE Dunn, D., Aoyagi, A., Barber, M., Becorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahrouf, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, W., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
 and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0570 row: 0 column: 18
 Seq primer: CGTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 22.
 Location/Qualifiers
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 /clone="UUGC1M0570018"
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 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid TUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (GI|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES

source

BASE COUNT 1 a 21 c 0 g 0 t
 ORIGIN
 Query Match 86.7%; Score 10.4; DB 28; Length 22;
 Best Local Similarity 91.7%; Pred.No. 7e+05; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GGGGTGGTGGG 12
 |||||
 Db 20 GGGGGGTGGGG 9
 Search completed: October 27, 2003, 13:59:29
 Job time : 1055.51 secs

AA928040 19 bp mRNA linear EST 22-APR-1998
 LOCUS o15809.s1 NCI_CGAP_HN4 Homo sapiens cDNA clone IMAGE:1486912 3'
 DEFINITION similar to TR:O04216 O04216 EXTENSIN ; contains element MSR1
 ACCESSION AA928040
 VERSION AA928040.1 GI:3077196
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 19)
 REFERENCE NCI/MDR-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 AUTHORS National Cancer Institute / National Institute of Dental Research,
 Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: John Ensley, M.D.
 cDNA Library Preparation: Stratagene, Inc.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Trace considered overall poor quality
 Seq primer: -48n13 fwd. 5T from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers
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 /db_xref="taxon:9606"
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 /tissue_type="squamous cell carcinoma"
 /lab_host="SOLR (kanamycin resistant)"
 /clone_lib="NCI_CGAP_HN4"
 /notes="Organ: pharynx; Vector: Bluescript SK-; Site: 1;
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)OACTAGCTCGAGTTTCTTTTCTTTT 3"
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 Best Local Similarity 100.0%; Pred.No. 1e+06;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 GGTGGTGGG 12
 |||||
 Db 3 GGTGGTGGG 12
 Search completed: October 27, 2003, 13:59:29
 Job time : 1055.51 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:34 ; Search time 27.5429 Seconds
(without alignments)
192.304 Million cell updates/sec

Title: US-09-331-204A-13
Perfect score: 12
Sequence: 1 ggggtggtggg 12

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 376294

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
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5: /cgn2_6/ptodata/1/ina/PTCUS COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	100.0	18	2	US-08-529-878B-3
2	12	100.0	18	2	US-08-529-878B-10
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4	12	100.0	18	2	US-08-529-878B-48
5	12	100.0	21	2	US-08-529-878B-4
6	12	100.0	21	2	US-08-529-878B-45
7	11	91.7	17	3	US-09-017-974-62
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10	11	91.7	17	4	US-08-682-255A-62
11	11	91.7	17	4	US-08-682-255A-64
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15	11	91.7	17	4	US-09-429-130-65
16	11	91.7	20	2	US-08-476-712-2
17	11	91.7	20	2	US-08-890-980-56
18	11	91.7	20	3	US-08-890-979-56
19	11	91.7	20	3	US-09-032-894-56
20	11	91.7	20	3	US-09-031-626-56
21	11	91.7	20	4	US-09-411-291-2
22	11	91.7	20	5	PCT-US93-07743-14
23	11	91.7	21	1	US-08-145-704-11
24	11	91.7	21	3	US-08-987-574-11
25	11	91.7	21	3	US-08-535-168-11
26	11	91.7	21	3	US-09-017-974-11
27	11	91.7	21	4	US-08-682-255A-11

28	11	91.7	21	4	US-09-429-130-11	Sequence 11, Appl
29	11	91.7	21	5	PCT-US96-11786-11	Sequence 11, Appl
30	10.4	86.7	15	1	US-08-580-242-2	Sequence 2, Appl
31	10.4	86.7	15	5	PCT-US94-06331A-22	Sequence 22, Appl
32	10.4	86.7	18	1	US-08-459-802B-13	Sequence 13, Appl
33	10.4	86.7	18	2	US-08-287-503B-31	Sequence 31, Appl
34	10.4	86.7	20	3	US-09-513-729B-63	Sequence 63, Appl
35	10.4	86.7	20	3	US-09-487-368A-174	Sequence 174, Appl
36	10.4	86.7	20	3	US-09-662-249A-20	Sequence 20, Appl
37	10.4	86.7	20	3	US-09-662-249A-21	Sequence 21, Appl
38	10.4	86.7	20	3	US-09-662-249A-22	Sequence 22, Appl
39	10.4	86.7	20	4	US-09-629-644A-174	Sequence 174, Appl
40	10.4	86.7	20	4	US-09-138-452A-3980	Sequence 3980, Appl
41	10.4	86.7	21	1	US-08-145-704-10	Sequence 10, Appl
42	10.4	86.7	21	3	US-08-987-574-10	Sequence 10, Appl
43	10.4	86.7	21	3	US-08-535-168-10	Sequence 10, Appl
44	10.4	86.7	21	3	US-09-017-974-10	Sequence 10, Appl
45	10.4	86.7	21	4	US-08-682-255A-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-529-878B-3
; Sequence 3, Application US/08529878B
; Patent No. 5932556
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESS: Crockett & Fish
; STREET: 3000 S. Augusta Court
; CITY: La Habra
; STATE: California
; COUNTRY: United States of America
; ZIP: 90631
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/529,878B
; FILING DATE: 13-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Fish, Robert D.
; REGISTRATION NUMBER: 33,980
; REFERENCE/DOCKET NUMBER: 213/003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-525-3433
; TELEFAX: 714-525-3303
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-529-878B-3

Query Match 100.0%; Score 12; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGTGGTGGG 12
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Db 7 GGGGTGGTGGG 18

RESULT 2
US-08-529-878B-10/C
; Sequence 10, Application US/08529878B
; Patent No. 5932556
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; REGULATION OF CD28 EXPRESSION
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Crockett & Fish
; STREET: 3000 S. Augusta Court
; CITY: La Habra
; STATE: California
; COUNTRY: United States of America
; ZIP: 90631
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/529,878B
; FILING DATE: 13-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Fish, Robert D.
; REGISTRATION NUMBER: 33,880
; REFERENCE/DOCKET NUMBER: 213/003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-525-3433
; TELEFAX: 714-525-3303
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-529-878B-10

Query Match 100.0%; Score 12; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGG 12
Db 18 GGGGTGGTGGG 7

RESULT 3
US-08-529-878B-44
; Sequence 44, Application US/08529878B
; Patent No. 5932556
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; REGULATION OF CD28 EXPRESSION
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Crockett & Fish
; STREET: 3000 S. Augusta Court
; CITY: La Habra
; STATE: California
; COUNTRY: United States of America
; ZIP: 90631
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/529,878B
; FILING DATE: 13-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Fish, Robert D.
; REGISTRATION NUMBER: 33,880
; REFERENCE/DOCKET NUMBER: 213/003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-525-3433
; TELEFAX: 714-525-3303
; TELEX:
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-529-878B-44

Query Match 100.0%; Score 12; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGG 12
Db 7 GGGGTGGTGGG 18

RESULT 4
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; Sequence 48, Application US/08529878B
; Patent No. 5932556
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; REGULATION OF CD28 EXPRESSION
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Crockett & Fish
; STREET: 3000 S. Augusta Court
; CITY: La Habra
; STATE: California
; COUNTRY: United States of America
; ZIP: 90631
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/529,878B
; FILING DATE: 13-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Fish, Robert D.
; REGISTRATION NUMBER: 33,880
; REFERENCE/DOCKET NUMBER: 213/003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-525-3433
; TELEFAX: 714-525-3303
; TELEX:
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-529-878B-48

Query Match

100.0%; Score 12; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGG 12
Db 18 GGGGTGGTGGG 7

RESULT 5

US-08-529-878B-4
; Sequence 4, Application US/08529878B
; Patent No. 5932556
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; REGULATION OF CD28 EXPRESSION
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Crockett & Fish
; STREET: 3000 S. Augusta Court
; CITY: La Habra
; STATE: California
; COUNTRY: United States of America
; ZIP: 90631

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/529,878B
; FILING DATE: 13-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Fish, Robert D.
; REGISTRATION NUMBER: 33,880
; REFERENCE/DOCKET NUMBER: 213/003
; TELEPHONE: 714-525-3433
; TELEFAX: 714-525-3303
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-529-878B-4

Query Match 100.0%; Score 12; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGG 12
Db 10 GGGGTGGTGGG 21

RESULT 6

US-08-529-878B-45
; Sequence 45, Application US/08529878B
; Patent No. 5932556
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; REGULATION OF CD28 EXPRESSION
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Crockett & Fish
; STREET: 3000 S. Augusta Court
; CITY: La Habra
; STATE: California

COUNTRY: United States of America
ZIP: 90631
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/529,878B
; FILING DATE: 13-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Fish, Robert D.
; REGISTRATION NUMBER: 33,880
; REFERENCE/DOCKET NUMBER: 213/003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-525-3433
; TELEFAX: 714-525-3303
; TELEX:
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-529-878B-45

Query Match 100.0%; Score 12; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGG 12
Db 10 GGGGTGGTGGG 21

RESULT 7

US-09-017-974-62
; Sequence 62, Application US/09017974
; Patent No. 6288042
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; APPLICANT: Ojwang, Joshua O.
; APPLICANT: Hogan, Michael E.
; APPLICANT: Wallace, Thomas L.
; APPLICANT: Cossam, Paul A.
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich
; Tetrad Forming Oligonucleotides
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Conley, Rose & Tayon, P.C.
; STREET: 600 Travis, Suite 1800
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77002-2912
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word 97 (saved as .txt file)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/017,974
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/037,374
; FILING DATE: 04-FEB-97
; APPLICATION NUMBER:
; FILING DATE: 09-DEC-97
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, C. Steven

/ REGISTRATION NUMBER: 33,962
/ REFERENCE/DOCKET NUMBER: 1472-06223
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 713/238-8010
/ TELEFAX: 713/238-8008
/ INFORMATION FOR SEQ ID NO: 62:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
US-09-017-974-62

Query Match 91.7%; Score 11; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0;

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Db 6 GGGGTGGTGGG 16

RESULT 8
US-09-017-974-64
; Sequence 64, Application US/09017974
; Patent No. 6288042
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; APPLICANT: Ojwang, Joshua O.
; APPLICANT: Hogan, Michael E.
; APPLICANT: Wallace, Thomas L.
; APPLICANT: Cossum, Paul A.
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich
; TITLE OF INVENTION: Tetrad Forming Oligonucleotides
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Conley, Rose & Tayon, P.C.
; STREET: 600 Travis, Suite 1800
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77002-2912
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/037,374
; FILING DATE: 04-FEB-97
; APPLICATION NUMBER:
; FILING DATE: 09-DEC-97
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, C. Steven
; REGISTRATION NUMBER: 33,962
; REFERENCE/DOCKET NUMBER: 1472-06223
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/238-8010
; TELEFAX: 713/238-8008
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-017-974-64

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Best Local Similarity 100.0%; Pred. No. 3.3e+03;
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Db 3 GGGGTGGTGGG 13

RESULT 9
US-09-017-974-65
; Sequence 65, Application US/09017974
; Patent No. 6288042
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; APPLICANT: Ojwang, Joshua O.
; APPLICANT: Hogan, Michael E.
; APPLICANT: Wallace, Thomas L.
; APPLICANT: Cossum, Paul A.
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich
; TITLE OF INVENTION: Tetrad Forming Oligonucleotides
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Conley, Rose & Tayon, P.C.
; STREET: 600 Travis, Suite 1800
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77002-2912
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; APPLICATION NUMBER: US/09/017,974
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/037,374
; FILING DATE: 04-FEB-97
; APPLICATION NUMBER:
; FILING DATE: 09-DEC-97
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, C. Steven
; REGISTRATION NUMBER: 33,962
; REFERENCE/DOCKET NUMBER: 1472-06223
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/238-8010
; TELEFAX: 713/238-8008
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 5
; OTHER INFORMATION: /note= "C-5 propynl dU"
US-09-017-974-65

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Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0;

Qy 1 GGGGTGGTGGG 11
Db 6 GGGGTGGTGGG 16

RESULT 10

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US-08-682-255A-62
; Sequence 62, Application US/08682255A
; Patent No. 6323185
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; APPLICANT: Fennwald, Susan
; APPLICANT: Zendequi, Joseph G.
; APPLICANT: Ojwang, Joshua O.
; APPLICANT: Hogan, Michael E.
; APPLICANT: Pommier, Yves
; APPLICANT: Mazunder, Abhijit
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESS: Conley, Rose & Tayon, P.C.
; STREET: 600 Travis, Suite 1850
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77002-2912
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS Windows 95
; SOFTWARE: MS Word 97 (saved as .txt file)
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; APPLICATION NUMBER: US/08/682,255A
; FILING DATE: 17-JULY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/535,168
; FILING DATE: 23-OCT-95
; APPLICATION NUMBER: 60/001,505
; FILING DATE: 19-JULY-95
; APPLICATION NUMBER: 60/014,007
; FILING DATE: 19-JULY-95
; APPLICATION NUMBER: 60/013,688
; FILING DATE: 25-MARCH-96
; APPLICATION NUMBER: 60/015,714
; FILING DATE: 19-MARCH-96
; APPLICATION NUMBER: 60/016,271
; FILING DATE: 23-APRIL-96
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, C. Steven
; REGISTRATION NUMBER: 33,962
; REFERENCE/DOCKET NUMBER: 1472-06214
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/238-8010
; TELEFAX: 713/238-8008
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-682-255A-62

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Query Match          91.7%; Score 11; DB 4; Length 17;
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 6 GGGGTGGTGGG 16

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RESULT 11
US-08-682-255A-64
; Sequence 64, Application US/08682255A
; Patent No. 6323185
; GENERAL INFORMATION:

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; APPLICANT: Rando, Robert F.
; APPLICANT: Fennwald, Susan
; APPLICANT: Zendequi, Joseph G.
; APPLICANT: Ojwang, Joshua O.
; APPLICANT: Hogan, Michael E.
; APPLICANT: Pommier, Yves
; APPLICANT: Mazunder, Abhijit
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESS: Conley, Rose & Tayon, P.C.
; STREET: 600 Travis, Suite 1850
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77002-2912
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS Windows 95
; SOFTWARE: MS Word 97 (saved as .txt file)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/682,255A
; FILING DATE: 17-JULY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/535,168
; FILING DATE: 23-OCT-95
; APPLICATION NUMBER: 60/001,505
; FILING DATE: 19-JULY-95
; APPLICATION NUMBER: 60/014,007
; FILING DATE: 25-MARCH-96
; APPLICATION NUMBER: 60/013,688
; FILING DATE: 19-MARCH-96
; APPLICATION NUMBER: 60/015,714
; FILING DATE: 17-APRIL-96
; APPLICATION NUMBER: 60/016,271
; FILING DATE: 23-APRIL-96
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, C. Steven
; REGISTRATION NUMBER: 33,962
; REFERENCE/DOCKET NUMBER: 1472-06214
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/238-8010
; TELEFAX: 713/238-8008
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-682-255A-64

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Query Match          91.7%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred.No. 3.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2 GGGGTGGTGGG 12
    |||||
Db 3 GGGGTGGTGGG 13

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RESULT 12
US-08-682-255A-65
; Sequence 65, Application US/08682255A
; Patent No. 6323185
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; APPLICANT: Fennwald, Susan
; APPLICANT: Zendequi, Joseph G.
; APPLICANT: Ojwang, Joshua O.

```

APPLICANT: Hogan, Michael E.
APPLICANT: Pommier, Yves
APPLICANT: Mazunder, Abhijit
TITLE OF INVENTION: Anti-Viral Guanosine-Rich
TITLE OF INVENTION: Oligonucleotides
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Conley, Rose & Tayon, P.C.
STREET: 600 Travis, Suite 1850
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77002-2912
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS Windows 95
SOFTWARE: MS Word 97 (saved as .txt file)
CURRENT APPLICATION DATA: US/08/692,255A
FILING DATE: 17-JULY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/535,168
FILING DATE: 23-OCT-95
APPLICATION NUMBER: 60/001,505
FILING DATE: 19-JULY-95
APPLICATION NUMBER: 60/014,007
FILING DATE: 25-MARCH-96
APPLICATION NUMBER: 60/013,688
FILING DATE: 19-MARCH-96
APPLICATION NUMBER: 60/015,714
FILING DATE: 17-APRIL-96
APPLICATION NUMBER: 60/016,271
FILING DATE: 23-APRIL-96
ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, C. Steven
REGISTRATION NUMBER: 33,962
REFERENCE/DOCKET NUMBER: 1472-06214
TELEPHONE: 713/238-8010
TELEFAX: 713/238-8008
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 5
OTHER INFORMATION: /note= "C-5 propynl dU"
US-08-682-255A-65

Query Match 91.7%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0;

Qy 1 GGGGTGGTGGG 11
Db 6 GGGGTGGTGGG 16

RESULT 13
US-09-429-130-62
Sequence 62, Application US/09429130
Patent No. 6355785
GENERAL INFORMATION:
APPLICANT: Rando, Robert F.
Fennewald, Susan
Zendequi, Joseph G.
Ojwang, Joshua O.

Hogan, Michael E.
Pommier, Yves
Mazunder, Abhijit
60/015,714
TITLE OF INVENTION: Anti-Viral Guanosine-Rich
TITLE OF INVENTION: Oligonucleotides
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Conley, Rose & Tayon, P.C.
STREET: 600 Travis, Suite 1850
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77002-2912
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS Windows 95
SOFTWARE: MS Word 97 (saved as .txt file)
CURRENT APPLICATION DATA: US/09/429,130
FILING DATE: 28-OCT-1999
CLASSIFICATION: <Unknown>
19-JULY-95
25-MARCH-96
19-MARCH-96
17-APRIL-96
23-APRIL-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/682,255
FILING DATE: <Unknown>
APPLICATION NUMBER: 60/001,505
FILING DATE: 19-JULY-95
APPLICATION NUMBER: 60/014,007
FILING DATE: 25-MARCH-96
APPLICATION NUMBER: 60/013,688
FILING DATE: 19-MARCH-96
APPLICATION NUMBER: 60/016,271
FILING DATE: 17-APRIL-96
ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, C. Steven
REGISTRATION NUMBER: 33,962
REFERENCE/DOCKET NUMBER: 1472-06214
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/238-8010
TELEFAX: 713/238-8008
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 62:
US-09-429-130-62

Query Match 91.7%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGG 11
Db 6 GGGGTGGTGGG 16

RESULT 14
US-09-429-130-64
Sequence 64, Application US/09429130
Patent No. 6355785
GENERAL INFORMATION:
APPLICANT: Rando, Robert F.
Fennewald, Susan
Zendequi, Joseph G.

Olwang, Joshua O.
Hogan, Michael E.
Pommier, Yves
Mazunder, Abhijit
60/015,714

TITLE OF INVENTION: Anti-Viral Guanosine-Rich
Oligonucleotides

NUMBER OF SEQUENCES: 87

CORRESPONDENCE ADDRESS:
ADDRESSEE: Conley, Rose & Tayon, P.C.
STREET: 600 Travis, Suite 1850
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77002-2912

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS Windows 95
SOFTWARE: MS Word 97 (saved as .txt file)

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19-JULY-95
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17-APRIL-96
23-APRIL-96

PRIOR APPLICATION DATA:
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FILING DATE: <Unknown>
APPLICATION NUMBER: 60/001,505
FILING DATE: 19-JULY-95
APPLICATION NUMBER: 60/014,007
FILING DATE: 25-MARCH-96
APPLICATION NUMBER: 60/013,688
FILING DATE: 19-MARCH-96
APPLICATION NUMBER: 60/016,271
FILING DATE: 17-APRIL-96

ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, C. Steven
REGISTRATION NUMBER: 33,962
REFERENCE/DOCKET NUMBER: 1472-06214

TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/238-8010
TELEFAX: 713/238-8008

INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 64:

US-09-429-130-64

Query Match 91.7%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 3 GGGTGTGGG 13

RESULT 15
US-09-429-130-65
Sequence 65, Application US/09/429130
Patent No. 6355785
GENERAL INFORMATION:
APPLICANT: Rando, Robert F.
Fennewald, Susan

Zendequi, Joseph G.
Olwang, Joshua O.
Hogan, Michael E.
Pommier, Yves
Mazunder, Abhijit
60/015,714

TITLE OF INVENTION: Anti-Viral Guanosine-Rich
Oligonucleotides

NUMBER OF SEQUENCES: 87

CORRESPONDENCE ADDRESS:
ADDRESSEE: Conley, Rose & Tayon, P.C.
STREET: 600 Travis, Suite 1850
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77002-2912

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS Windows 95
SOFTWARE: MS Word 97 (saved as .txt file)

CURRENT APPLICATION DATA:
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FILING DATE: 28-Oct-1999
CLASSIFICATION: <Unknown>
19-JULY-95
25-MARCH-96
19-MARCH-96
17-APRIL-96
23-APRIL-96

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/682,255
FILING DATE: <Unknown>
APPLICATION NUMBER: 60/001,505
FILING DATE: 19-JULY-95
APPLICATION NUMBER: 60/014,007
FILING DATE: 25-MARCH-96
APPLICATION NUMBER: 60/013,688
FILING DATE: 19-MARCH-96
APPLICATION NUMBER: 60/016,271
FILING DATE: 17-APRIL-96

ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, C. Steven
REGISTRATION NUMBER: 33,962
REFERENCE/DOCKET NUMBER: 1472-06214

TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/238-8010
TELEFAX: 713/238-8008

INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

FEATURE:
NAME/KEY: misc_feature
LOCATION: 5
OTHER INFORMATION: /note= "C-5 propynl du"

SEQUENCE DESCRIPTION: SEQ ID NO: 65:

US-09-429-130-65

Query Match 91.7%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 6 GGGGTGTGGG 16

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Job time : 28.5429 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 11:25:34 ; Search time 258.629 Seconds
(without alignments)
124.432 Million cell updates/sec

Title: US-09-331-204A-13

Perfect score: 12

Sequence: 1 999gtggtg99g 12

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Maximum DB seq length: 22

Post-processing: Minimum Match 0%

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Listing first 45 summaries

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SUMMARIES

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C 10	11	91.7	20	14	US-09-779-152-56
C 11	11	91.7	20	14	US-10-023-610-56
C 12	11	91.7	21	12	US-10-184-085A-365
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C 16	11	91.7	21	12	US-10-184-085A-370

C 17	11	91.7	21	12	US-10-184-085A-371	Sequence 371, App
C 18	11	91.7	21	12	US-10-184-085A-373	Sequence 373, App
C 19	11	91.7	21	12	US-10-184-085A-374	Sequence 374, App
C 20	11	91.7	21	12	US-10-184-085A-375	Sequence 375, App
C 21	11	91.7	21	12	US-10-184-085A-376	Sequence 376, App
C 22	11	91.7	21	12	US-10-184-085A-405	Sequence 405, App
C 23	11	91.7	21	12	US-10-184-085A-408	Sequence 408, App
C 24	11	91.7	21	12	US-10-184-085A-506	Sequence 506, App
C 25	11	91.7	21	12	US-10-148-887-38	Sequence 38, Appl
C 26	10.4	86.7	17	11	US-09-780-533A-49	Sequence 49, Appl
C 27	10.4	86.7	17	11	US-09-780-533A-932	Sequence 932, App
C 28	10.4	86.7	17	11	US-09-780-533A-933	Sequence 933, App
C 29	10.4	86.7	17	11	US-09-780-533A-934	Sequence 934, App
C 30	10.4	86.7	17	11	US-09-780-533A-935	Sequence 935, App
C 31	10.4	86.7	17	11	US-09-848-754A-2390	Sequence 2390, App
C 32	10.4	86.7	17	11	US-09-848-754A-2869	Sequence 2869, App
C 33	10.4	86.7	17	11	US-09-848-754A-3378	Sequence 3378, App
C 34	10.4	86.7	17	11	US-09-848-754A-3379	Sequence 3379, App
C 35	10.4	86.7	17	12	US-10-238-700-446	Sequence 446, App
C 36	10.4	86.7	17	12	US-10-238-700-447	Sequence 447, App
C 37	10.4	86.7	19	12	US-10-251-117-671	Sequence 671, App
C 38	10.4	86.7	19	12	US-10-251-117-978	Sequence 978, App
C 39	10.4	86.7	20	9	US-09-854-883-174	Sequence 174, App
C 40	10.4	86.7	20	11	US-09-904-968A-105	Sequence 105, App
C 41	10.4	86.7	20	12	US-10-083-246A-118	Sequence 118, App
C 42	10.4	86.7	22	12	US-10-214-417A-32	Sequence 32, Appl
C 43	10.4	86.7	22	12	US-10-214-417A-35	Sequence 35, Appl
C 44	10	83.3	16	14	US-10-206-839-38	Sequence 38, Appl
C 45	10	83.3	19	12	US-10-240-046A-62	Sequence 62, Appl

ALIGNMENTS

RESULT 1

US-09-740-332-2132/c
; Sequence 2132, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2132
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-2132

Query Match 100.0%; Score 12; DB 11; Length 17;
Best Local Similarity 100.0%; Pred No. 9e+03; 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGGG 12

Db 16 GGGGTGGTGGGG 5

RESULT 2

US-09-740-332-2133/c
; Sequence 2133, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat

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; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2133
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-2133

```

```

Query Match          100.0%; Score 12; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 GGGGTGGTGGG 12
    |||||
Db 13 GGGGTGGTGGG 2

```

```

RESULT 3
US-09-740-332-2422
; Sequence 2422, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2422
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-2422

```

```

Query Match          100.0%; Score 12; DB 11; Length 17;
Best Local Similarity 83.3%; Pred. No. 9e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 GGGGTGGTGGG 12
    |||||
Db 6 GGGGUGGUGGGG 17

```

```

RESULT 4
US-09-740-332-2423
; Sequence 2423, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2423
; LENGTH: 17
; TYPE: RNA

```

```

; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-2423

```

```

Query Match          100.0%; Score 12; DB 11; Length 17;
Best Local Similarity 83.3%; Pred. No. 9e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 GGGGTGGTGGG 12
    |||||
Db 3 GGGGUGGUGGGG 14

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```

RESULT 5
US-09-817-879-2132/c
; Sequence 2132, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MEH00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2132
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-2132

```

```

Query Match          100.0%; Score 12; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 GGGGTGGTGGG 12
    |||||
Db 16 GGGGTGGTGGG 5

```

```

RESULT 6
US-09-817-879-2133/c
; Sequence 2133, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MEH00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2133
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-2133

```

```

Query Match          100.0%; Score 12; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 9e+03;

```

```

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGTGGTGGGG 12
    |||||
Db 13 GGGGTGGTGGGG 2

RESULT 7
US-09-817-879-2422
; Sequence 2422, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; FILE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: MHB00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2422
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-2422

Query Match 100.0%; Score 12; DB 12; Length 17;
Best Local Similarity 83.3%; Pred. No. 9e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGGG 12
    |||||
Db 6 GGGGUGGUGGGG 17

RESULT 8
US-09-817-879-2423
; Sequence 2423, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; FILE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: MHB00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2423
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-2423

Query Match 100.0%; Score 12; DB 12; Length 17;
Best Local Similarity 83.3%; Pred. No. 9e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGGG 12
    |||||
Db 3 GGGGUGGUGGGG 14

RESULT 9
US-10-148-687-39/c
; Sequence 39, Application US/10148687
; Publication No. US20030185836A1
; GENERAL INFORMATION:
; APPLICANT: WINTER, Gerhard
; APPLICANT: SLADE, Martin Basil
; APPLICANT: WILLIAMS, Keith Leslie
; APPLICANT: GOOLEY, Andrew Arthur
; TITLE OF INVENTION: Cryptosporidium sporozoite antigens
; FILE REFERENCE: 047763-5019-US
; CURRENT APPLICATION NUMBER: US/10/148,687
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: PCT/AU00/01492
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: AU PQ4400
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primers
US-10-148-687-39

Query Match 91.7%; Score 11; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGTGGTGGGG 12
    |||||
Db 17 GGGTGGTGGGG 7

RESULT 10
US-09-779-152-56/c
; Sequence 56, Application US/09779152
; Publication No. US20030044782A1
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: O'Carroll, Jose M.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MNI-172CP2
; CURRENT APPLICATION NUMBER: US/09/779,152
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 08/890,979
; PRIOR FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-779-152-56

Query Match 91.7%; Score 11; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 11
    |||||
Db 13 GGGGTGGTGGG 3

RESULT 11
US-10-023-610-56/c
; Sequence 56, Application US/10023610
; Publication No. US20030023059A1
; GENERAL INFORMATION:

```

; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: SR-BI NUCLEIC ACIDS AND USES THEREFOR
; FILE REFERENCE: MIA-005.03
; CURRENT APPLICATION NUMBER: US/10/023,610
; EARLIER FILING DATE: 2001-12-17
; EARLIER APPLICATION NUMBER: 09/686,106
; EARLIER FILING DATE: 2000-10-10
; EARLIER APPLICATION NUMBER: 09/032,894
; EARLIER FILING DATE: 1998-02-27
; EARLIER APPLICATION NUMBER: 08/890,980
; EARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-10-023-610-56

Query Match 91.7%; Score 11; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGG 11
Db 13 GGGGTGGTGGG 3

RESULT 12

US-10-184-085A-365/c
; Sequence 365, Application US/10184085A
; Publication No. US20030152950A1
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Minna, John D.
; APPLICANT: Luebke, Kevin, J.
; APPLICANT: Balog, Robert P.
; TITLE OF INVENTION: Identification of Chemically Modified Polymers
; FILE REFERENCE: 119929-1035
; CURRENT APPLICATION NUMBER: US/10/184,085A
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/301,370
; PRIOR FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 1291
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 365
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-184-085A-365

Query Match 91.7%; Score 11; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGTGGTGGG 12
Db 21 GGGTGGTGGG 11

RESULT 13

US-10-184-085A-366/c
; Sequence 366, Application US/10184085A
; Publication No. US20030152950A1
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Minna, John D.
; APPLICANT: Luebke, Kevin, J.
; APPLICANT: Balog, Robert P.
; TITLE OF INVENTION: Identification of Chemically Modified Polymers
; FILE REFERENCE: 119929-1035
; CURRENT APPLICATION NUMBER: US/10/184,085A
; CURRENT FILING DATE: 2002-10-01

; PRIOR APPLICATION NUMBER: US 60/301,370
; PRIOR FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 1291
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 366
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-184-085A-366

Query Match 91.7%; Score 11; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGG 11
Db 21 GGGGTGGTGGG 11

RESULT 14

US-10-184-085A-367/c
; Sequence 367, Application US/10184085A
; Publication No. US20030152950A1
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Minna, John D.
; APPLICANT: Luebke, Kevin, J.
; APPLICANT: Balog, Robert P.
; TITLE OF INVENTION: Identification of Chemically Modified Polymers
; FILE REFERENCE: 119929-1035
; CURRENT APPLICATION NUMBER: US/10/184,085A
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/301,370
; PRIOR FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 1291
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 367
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-184-085A-367

Query Match 91.7%; Score 11; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGG 11
Db 20 GGGGTGGTGGG 10

RESULT 15

US-10-184-085A-368/c
; Sequence 368, Application US/10184085A
; Publication No. US20030152950A1
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Minna, John D.
; APPLICANT: Luebke, Kevin, J.
; APPLICANT: Balog, Robert P.
; TITLE OF INVENTION: Identification of Chemically Modified Polymers
; FILE REFERENCE: 119929-1035
; CURRENT APPLICATION NUMBER: US/10/184,085A
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/301,370
; PRIOR FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 1291
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 368
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-184-085A-368

Query Match 91.7%; Score 11; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGGTGGTGGG 11
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Db 19 GGGGTGGTGGG 9

Search completed: October 27, 2003, 19:00:53
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:35 ; Search time 1570.86 Seconds
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Title: US-09-331-204A-13
Perfect score: 12
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Gapop 10.0 , Gapext 1.0

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- 76: /cgn2_6/ptodata/1/pna/US6022_COMB.seq.*
- 77: /cgn2_6/ptodata/1/pna/US6023A_COMB.seq.*
- 78: /cgn2_6/ptodata/1/pna/US6023B_COMB.seq.*
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- 83: /cgn2_6/ptodata/1/pna/US6028_COMB.seq.*
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- 85: /cgn2_6/ptodata/1/pna/US6030_COMB.seq.*
- 86: /cgn2_6/ptodata/1/pna/US6031_COMB.seq.*
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- 88: /cgn2_6/ptodata/1/pna/US6033_COMB.seq.*
- 89: /cgn2_6/ptodata/1/pna/US6034_COMB.seq.*
- 90: /cgn2_6/ptodata/1/pna/US6035_COMB.seq.*
- 91: /cgn2_6/ptodata/1/pna/US6036_COMB.seq.*
- 92: /cgn2_6/ptodata/1/pna/US6037_COMB.seq.*
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- 94: /cgn2_6/ptodata/1/pna/US6039_COMB.seq.*
- 95: /cgn2_6/ptodata/1/pna/US6040_COMB.seq.*
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- 97: /cgn2_6/ptodata/1/pna/US6042_COMB.seq.*
- 98: /cgn2_6/ptodata/1/pna/US6043_COMB.seq.*
- 99: /cgn2_6/ptodata/1/pna/US6044_COMB.seq.*
- 100: /cgn2_6/ptodata/1/pna/US6045_COMB.seq.*
- 101: /cgn2_6/ptodata/1/pna/US6046_COMB.seq.*
- 102: /cgn2_6/ptodata/1/pna/US6047_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	12	100.0	12	19	US-09-331-204-3
2	12	100.0	12	19	US-09-331-204A-13
3	12	100.0	15	1	PCT-US01-21306-49
4	12	100.0	15	2	PCT-US01-21306-49

Sequence 3, Appli
Sequence 13, Appli
Sequence 49, Appli

C 5 12 100.0 17 32 US-09-740-332-2132 Sequence 2132, Ap
C 6 12 100.0 17 32 US-09-740-332-2133 Sequence 2133, Ap
C 7 12 100.0 17 32 US-09-740-332-2422 Sequence 2422, Ap
C 8 12 100.0 17 32 US-09-740-332-2423 Sequence 2423, Ap
C 9 12 100.0 17 34 US-09-817-879-2132 Sequence 2132, Ap
C 10 12 100.0 17 34 US-09-817-879-2133 Sequence 2133, Ap
C 11 12 100.0 17 34 US-09-817-879-2422 Sequence 2422, Ap
C 12 12 100.0 17 34 US-09-817-879-2423 Sequence 2423, Ap
C 13 12 100.0 17 50 US-10-303-778-13820 Sequence 13820, A
C 14 12 100.0 18 8 US-08-387-041A-3 Sequence 3, Appli
C 15 12 100.0 18 8 US-08-387-041A-10 Sequence 10, Appli
C 16 12 100.0 18 19 US-09-331-204-1 Sequence 1, Appli
C 17 12 100.0 18 19 US-09-331-204A-4 Sequence 4, Appli
C 18 12 100.0 18 19 US-09-331-204A-21 Sequence 21, Appli
C 19 12 100.0 18 33 US-08-786-436-17 Sequence 17, Appli
C 20 12 100.0 18 33 US-09-786-436-42 Sequence 42, Appli
C 21 12 100.0 18 50 US-10-310-188-9770 Sequence 9770, Ap
C 22 12 100.0 18 50 US-10-310-188-72857 Sequence 72857, A
C 23 12 100.0 19 49 US-10-293-338-6664 Sequence 6664, A
C 24 12 100.0 19 50 US-10-310-188-46976 Sequence 46976, A
C 25 12 100.0 19 50 US-10-310-188-64788 Sequence 64788, A
C 26 12 100.0 20 50 US-10-303-778-16088 Sequence 16088, A
C 27 12 100.0 20 50 US-10-310-188-31313 Sequence 31313, A
C 28 12 100.0 20 50 US-10-310-188-78501 Sequence 78501, A
C 29 12 100.0 21 8 US-08-387-041A-4 Sequence 4, Appli
C 30 12 100.0 21 19 US-09-331-204-6 Sequence 6, Appli
C 31 12 100.0 21 19 US-09-331-204A-6 Sequence 6, Appli
C 32 12 100.0 21 49 US-10-293-338-2091 Sequence 2091, Ap
C 33 12 100.0 21 50 US-10-310-188-31329 Sequence 31329, A
C 34 12 100.0 21 50 US-10-310-188-72837 Sequence 72837, A
C 35 12 100.0 21 50 US-10-310-188-78761 Sequence 78761, A
C 36 12 100.0 22 50 US-10-310-188-42141 Sequence 42141, A
C 37 11.6 96.7 15 1 PCT-US01-21306-48 Sequence 48, Appli
C 38 11.6 96.7 15 2 PCT-US01-21306-49 Sequence 49, Appli
C 39 11 91.7 17 1 PCT-US96-11786B-62 Sequence 62, Appli
C 40 11 91.7 17 1 PCT-US96-11786B-64 Sequence 64, Appli
C 41 11 91.7 17 1 PCT-US96-11786B-65 Sequence 65, Appli
C 42 11 91.7 17 1 PCT-US98-01974-62 Sequence 62, Appli
C 43 11 91.7 17 1 PCT-US98-01974-64 Sequence 64, Appli
C 44 11 91.7 17 1 PCT-US98-01974-65 Sequence 65, Appli
C 45 11 91.7 17 2 PCT-US96-11786B-62 Sequence 62, Appli

ALIGNMENTS

RESULT 1
US-09-331-204-3
; Sequence 3, Application US/09331204
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert
; TITLE OF INVENTION: G-RICH OLIGO APTAMERS AND METHODS OF MODULATING AN
; FILE REFERENCE: ICNSequence
; CURRENT APPLICATION NUMBER: US/09/331,204
; CURRENT FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US97/23927
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: An oligomer
; OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic
; OTHER INFORMATION: acid. This term includes oligomers consisting of
; OTHER INFORMATION: naturally occurring bases, sugars and intersugar (

Query Match 100.0%; Score 12; DB 19; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 2132, Ap
Sequence 2133, Ap
Sequence 2422, Ap
Sequence 2423, Ap
Sequence 2132, Ap
Sequence 2133, Ap
Sequence 2422, Ap
Sequence 2423, Ap
Sequence 13820, A
Sequence 3, Appli
Sequence 10, Appli
Sequence 4, Appli
Sequence 21, Appli
Sequence 17, Appli
Sequence 42, Appli
Sequence 9770, Ap
Sequence 72857, A
Sequence 6664, A
Sequence 46976, A
Sequence 64788, A
Sequence 16088, A
Sequence 31313, A
Sequence 78501, A
Sequence 4, Appli
Sequence 6, Appli
Sequence 2091, Ap
Sequence 31329, A
Sequence 72837, A
Sequence 78761, A
Sequence 42141, A
Sequence 48, Appli
Sequence 49, Appli
Sequence 62, Appli
Sequence 64, Appli
Sequence 65, Appli
Sequence 62, Appli
Sequence 64, Appli
Sequence 65, Appli
Sequence 62, Appli

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGGTGGTGGG 12
Db 1 GGGGTGGTGGG 12
RESULT 2
US-09-331-204A-13
; Sequence 13, Application US/09331204A
; GENERAL INFORMATION:
; APPLICANT: ICN Pharmaceuticals, Inc.
; APPLICANT: Tam, Robert
; TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Res
; FILE REFERENCE: 216/013-US1
; CURRENT APPLICATION NUMBER: US/09/331,204A
; CURRENT FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US97/23927
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 12
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-331-204A-13
Query Match 100.0%; Score 12; DB 19; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGGTGGTGGG 12
Db 1 GGGGTGGTGGG 12
RESULT 3
PCT-US01-21306-49
; Sequence 49, Application PC/TUS0121306
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Bentivegna, Steven C
; APPLICANT: Blegiecki, Karyn M.
; APPLICANT: Kazemi, Amir
; APPLICANT: Koshy, Beena
; TITLE OF INVENTION: Haplotypes of the E7FB Gene
; FILE REFERENCE: MMH-0902PCT E7FB
; CURRENT APPLICATION NUMBER: PCT/US01/21306
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/215,984
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-21306-49
Query Match 100.0%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGGTGGTGGG 12
Db 2 GGGGTGGTGGG 13
RESULT 4
PCT-US01-21306-49
; Sequence 49, Application PC/TUS0121306
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.

; APPLICANT: Bentivegna, Steven C
; APPLICANT: Bieglecki, Karyn M.
; APPLICANT: Kazemi, Amir
; APPLICANT: Koshiy, Beena
; TITLE OF INVENTION: Haplotypes of the ETPB Gene
; FILE REFERENCE: MW-0902PCT ETPB
; CURRENT APPLICATION NUMBER: PCT/US01/21306
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/215,984
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-21306-49

Query Match 100.0%; Score 12; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGGG 12
| | | | | | | | | |
Db 2 GGGGTGGTGGGG 13

RESULT 5

US-09-740-332-2132/c
; Sequence 2132, Application US/09740332
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2132
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-2132

Query Match 100.0%; Score 12; DB 32; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGGG 12
| | | | | | | | | |
Db 16 GGGGTGGTGGGG 5

RESULT 6

US-09-740-332-2133/c
; Sequence 2133, Application US/09740332
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2133
; LENGTH: 17
; TYPE: RNA

; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-2133

Query Match 100.0%; Score 12; DB 32; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGGG 12
| | | | | | | | | |
Db 13 GGGGTGGTGGGG 2

RESULT 7

US-09-740-332-2422
; Sequence 2422, Application US/09740332
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2422
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-2422

Query Match 100.0%; Score 12; DB 32; Length 17;
Best Local Similarity 83.3%; Pred. No. 8.7e+04;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGGG 12
| | | | | | | | | |
Db 6 GGGGTGGTGGGG 17

RESULT 8

US-09-740-332-2423
; Sequence 2423, Application US/09740332
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2423
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-2423

Query Match 100.0%; Score 12; DB 32; Length 17;
Best Local Similarity 83.3%; Pred. No. 8.7e+04;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 12
Db 3 GGGGUGUGGGG 14

RESULT 9

US-09-817-879-2132/c
; Sequence 2132, Application US/09817879
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: MBH00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2132
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-2132

Query Match 100.0%; Score 12; DB 34; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 12
Db 16 GGGGTGGTGGG 5

RESULT 10

US-09-817-879-2133/c
; Sequence 2133, Application US/09817879
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: MBH00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2133
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-2133

Query Match 100.0%; Score 12; DB 34; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 12
Db 13 GGGGTGGTGGG 2

RESULT 11

US-09-817-879-2422
; Sequence 2422, Application US/09817879
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate

; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: MBH00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2422
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-2422

Query Match 100.0%; Score 12; DB 34; Length 17;
Best Local Similarity 83.3%; Pred. No. 8.7e+04;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 12
Db 6 GGGGUGUGGGG 17

RESULT 12

US-09-817-879-2423
; Sequence 2423, Application US/09817879
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: MBH00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2423
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-2423

Query Match 100.0%; Score 12; DB 34; Length 17;
Best Local Similarity 83.3%; Pred. No. 8.7e+04;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGG 12
Db 3 GGGGUGUGGGG 14

RESULT 13

US-10-303-778-13820
; Sequence 13820, Application US/10303778
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL
; TITLE OF INVENTION: REGULATORY GENES AND USES THEREOF
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/10/303,778
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 17608
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13820
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-778-13820

Query Match 100.0%; Score 12; DB 50; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGG 12
Db 6 GGGGTGGTGGG 17

RESULT 14

US-08-387-041A-3
; Sequence 3, Application US/08387041A
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATION
; TITLE OF INVENTION: OF CD28 EXPRESSION
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,041A
; FILING DATE: 02-FEB-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8250-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-387-041A-3

Query Match 100.0%; Score 12; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGG 12
Db 7 GGGGTGGTGGG 18

RESULT 15

US-08-387-041A-10/C
; Sequence 10, Application US/08387041A
; GENERAL INFORMATION:
; APPLICANT: Tam, Robert C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATION
; TITLE OF INVENTION: OF CD28 EXPRESSION
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York

; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,041A
; FILING DATE: 02-FEB-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8250-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-387-041A-10

Query Match 100.0%; Score 12; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.8e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGG 12
Db 18 GGGGTGGTGGG 7

Search completed: October 27, 2003, 17:52:54
Job time: 1570.86 secs

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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 11:09:34 ; Search time 204.696 Seconds
(without alignments)
97.777 Million cell updates/sec

Title: US-09-331-204A-13

Perfect score: 12

Sequence: 1 999gtggtg99g 12

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2231628 seqs, 833900706 residues

Total number of hits satisfying chosen parameters: 264402

Minimum DB seq length: 0

Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 1: /cgn2_6/ptodata/1/pna/PTC_NEW_COMB.seq:*
 - 2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
 - 3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
 - 4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
 - 5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
 - 6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
 - 7: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	12	100.0	17	6	US-10-669-841-4725
C 3	12	100.0	17	6	US-10-669-841-5015
4	12	100.0	17	6	US-10-669-841-5016
5	12	100.0	18	1	PT-US02-38216-9770
6	12	100.0	18	1	PT-US02-38216-72857
7	12	100.0	19	1	PT-US02-38216-46976
8	12	100.0	19	1	PT-US02-38216-64788
9	12	100.0	20	1	PT-US02-38216-31313
10	12	100.0	20	1	PT-US02-38216-78501
11	12	100.0	21	1	PT-US02-38216-31329
12	12	100.0	21	1	PT-US02-38216-72837
13	12	100.0	21	1	PT-US02-38216-78761
14	12	100.0	22	1	PT-US02-38216-42141
15	11	91.7	17	1	PT-US02-38216-39287
16	11	91.7	18	1	PT-US02-38216-10573
17	11	91.7	18	1	PT-US02-38216-31330
18	11	91.7	18	1	PT-US02-38216-56500
19	11	91.7	18	5	US-09-943-944E-22
20	11	91.7	19	1	PT-US02-38216-78687
21	11	91.7	20	1	PT-US02-38216-10564
22	11	91.7	20	1	PT-US02-38216-41184
23	11	91.7	20	1	PT-US02-38216-63924
24	11	91.7	20	1	PT-US02-38216-64021
25	11	91.7	20	1	PT-US02-38216-64022
26	11	91.7	20	5	US-09-978-333B-2

27	11	91.7	20	5	US-09-978-333C-2
28	11	91.7	22	1	PT-US02-38216-39252
29	11	91.7	22	1	PT-US02-38216-63970
30	11	91.7	22	1	PT-US02-38216-83087
31	10.4	86.7	15	1	PT-US02-38216-34808
32	10.4	86.7	15	1	PT-US02-38216-72787
33	10.4	86.7	15	1	PT-US02-38216-84942
34	10.4	86.7	15	1	PT-US02-38216-84968
35	10.4	86.7	16	1	PT-US02-38216-9718
36	10.4	86.7	16	1	PT-US02-38216-31332
37	10.4	86.7	16	1	PT-US02-38216-51833
38	10.4	86.7	16	1	PT-US02-38216-60635
39	10.4	86.7	16	1	PT-US02-38216-61028
40	10.4	86.7	16	1	PT-US02-38216-64024
41	10.4	86.7	16	1	PT-US02-38216-72823
42	10.4	86.7	16	1	PT-US02-38216-73073
43	10.4	86.7	16	1	PT-US02-38216-75530
44	10.4	86.7	17	1	PT-US02-38216-9811
45	10.4	86.7	17	1	PT-US02-38216-26671

ALIGNMENTS

RESULT 1
US-10-669-841-4725/c
; Sequence 4725, Application US/10669841
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patricia, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEI
; FILE REFERENCE: 400/042US (MEHB02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4725
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; FEATURE:
; NAME/KEY: misc_feature

; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-10-669-841-4725

Query Match 100.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGG 12
Db 16 GGGGTGGTGGG 5

RESULT 2

US-10-669-841-4726/c
; Sequence 4726 Application US/10669841
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patrice, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEP
; FILE REFERENCE: 400/042US (MEHB02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 4726
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-10-669-841-4726

Query Match 100.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGG 12
Db 13 GGGGTGGTGGG 2

RESULT 3

US-10-669-841-5015
; Sequence 5015 Application US/10669841
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patrice, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HE
; FILE REFERENCE: 400/042US (MEHB02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 5015
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-10-669-841-5015

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Best Local Similarity 83.3%; Pred. No. 1.4e+04;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGG 12
Db 6 GGGGTGGTGGG 17

RESULT 4

US-10-669-841-5016
; Sequence 5016 Application US/10669841
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey

Matches	12;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	GGGGTGGTGGG	12						
Db	2	GGGGTGGTGGG	13						
RESULT 6									
PCT-US02-38216-72857									
; Sequence 72857, Application PC/TUS0238216									
; GENERAL INFORMATION:									
; APPLICANT: Rosetta Genomics LTD									
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY									
; TITLE OF INVENTION: GENES AND USES THEREOF									
; FILE REFERENCE: 55002									
; CURRENT APPLICATION NUMBER: PCT/US02/38216									
; CURRENT FILING DATE: 2002-11-12									
; NUMBER OF SEQ ID NOS: 86841									
; SOFTWARE: PatentIn version 3.2									
; SEQ ID NO 72857									
; LENGTH: 18									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
PCT-US02-38216-72857									
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Best Local Similarity 100.0%; Pred. No. 1.4e+04;									
Matches	12;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	GGGGTGGTGGG	12						
Db	1	GGGGTGGTGGG	12						
RESULT 7									
PCT-US02-38216-46976									
; Sequence 46976, Application PC/TUS0238216									
; GENERAL INFORMATION:									
; APPLICANT: Rosetta Genomics LTD									
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY									
; TITLE OF INVENTION: GENES AND USES THEREOF									
; FILE REFERENCE: 55002									
; CURRENT APPLICATION NUMBER: PCT/US02/38216									
; CURRENT FILING DATE: 2002-11-12									
; NUMBER OF SEQ ID NOS: 86841									
; SOFTWARE: PatentIn version 3.2									
; SEQ ID NO 46976									
; LENGTH: 19									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
PCT-US02-38216-46976									
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Best Local Similarity 100.0%; Pred. No. 1.4e+04;									
Matches	12;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	GGGGTGGTGGG	12						
Db	8	GGGGTGGTGGG	19						
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; Sequence 64788, Application PC/TUS0238216									
; GENERAL INFORMATION:									
; APPLICANT: Rosetta Genomics LTD									
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY									
; TITLE OF INVENTION: GENES AND USES THEREOF									
; FILE REFERENCE: 55002									
; CURRENT APPLICATION NUMBER: PCT/US02/38216									
; CURRENT FILING DATE: 2002-11-12									
; NUMBER OF SEQ ID NOS: 86841									
; SOFTWARE: PatentIn version 3.2									

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; SEQ ID NO 64798
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-64798

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Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGGG 12
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Db 14 GGGGTGGTGGGG 3

RESULT 9
PCT-US02-38216-31313
; Sequence 31313, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31313
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-31313

Query Match      100.0%; Score 12; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGGG 12
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Db 1 GGGGTGGTGGGG 12

RESULT 10
PCT-US02-38216-78501
; Sequence 78501, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 78501
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-78501

Query Match      100.0%; Score 12; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGGG 12
    |||||
Db 6 GGGGTGGTGGGG 17

RESULT 11
PCT-US02-38216-31329
; Sequence 31329, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31329
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-31329

Query Match      100.0%; Score 12; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGGG 12
    |||||
Db 1 GGGGTGGTGGGG 12

RESULT 12
PCT-US02-38216-72837
; Sequence 72837, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 72837
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-72837

Query Match      100.0%; Score 12; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGGG 12
    |||||
Db 1 GGGGTGGTGGGG 12

RESULT 13
PCT-US02-38216-78761
; Sequence 78761, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 78761
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-78761

Query Match      100.0%; Score 12; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGGTGGGG 12
    |||||
Db 8 GGGGTGGTGGGG 19
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Db 9 GGGGTGGTGGG 20
|||||

RESULT 14

PCT-US02-38216-42141
; Sequence 42141, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42141
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-42141

Query Match 100.0%; Score 12; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGGG 12
|||||
Db 6 GGGGTGGTGGG 17

RESULT 15

PCT-US02-38216-39287
; Sequence 39287, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39287
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-39287

Query Match 91.7%; Score 11; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 7 GGGGTGGTGGG 17

Search completed: October 27, 2003, 18:22:56
Job time : 205.686 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:29 ; Search time 162 Seconds

(without alignments)
299.938 Million cell updates/sec

Title: US-09-331-204A-8

Perfect score: 18

Sequence: 1 ttgaggggaggtg999.18

Scoring table: IDENTITY NUC

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Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 1643890

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	18	100.0	18	AAT36243	CD28 expression in
2	18	100.0	18	AAAX90336	CD28 inhibiting ph
3	16.4	91.1	18	AAT36242	CD28 expression in
4	16.4	91.1	18	AAT36196	Triplex forming ol
5	16.4	91.1	18	AAAX90328	CD28 inhibiting ph
6	16.4	91.1	18	AAAX90335	CD28 inhibiting ph
7	16.4	91.1	18	AAAX90290	CD28 inhibition ol
8	16.4	91.1	18	AAZ99625	Nucleotide sequenc

C	9	16.4	91.1	18	21	AAZ99650	Nucleotide sequenc
	10	16.4	91.1	21	17	AAT36197	Triplex forming ol
	11	16.4	91.1	21	20	AAAX90329	CD28 inhibiting ph
	12	16.4	91.1	21	20	AAAX90291	CD28 inhibition ol
	13	14.8	82.2	22	22	AAAF16593	Gastric acid produ
	14	14.8	80.0	22	22	AAAF01954	Hammerhead ribozym
	15	13.8	76.7	20	22	AAAD11117	Rat PTP1B antisens
	16	13.8	76.7	20	24	ABK85192	Rat PTP1B antisens
	17	13.8	76.7	20	24	ABK85192	Rat PTP1B antisens
	18	13.8	76.7	21	11	AAQ06932	MMY24 nucleotide c
	19	13.8	76.7	21	18	AAT98040	Human or simian im
	20	13.4	74.4	17	24	ABV91221	Human POSHL1 scann
	21	13.4	74.4	17	24	ABV91222	Human POSHL1 scann
	22	13.4	74.4	17	24	ABV91223	Human POSHL1 scann
	23	13.4	74.4	19	17	AAAS6945	HIV-1 proviral DNA
	24	13.4	74.4	19	24	AAAD41090	Primer ON-DHPR-F1
	25	13.4	74.4	19	24	ABT03925	Human pol kappa 76
	26	13.4	74.4	20	21	AAZ75053	Human biallelic ma
	27	13.2	73.3	18	17	AAT36244	CD28 expression in
	28	13.2	73.3	18	20	AAAX90337	CD28 inhibiting ph
	29	13.2	73.3	21	24	ABK93294	Hepatitis C virus
	30	13	72.2	20	24	ABT08387	Human CC3 promoter
	31	12.8	71.1	17	20	AAAL4740	Triple helix formi
	32	12.8	71.1	17	20	AAV55680	Human tissue kall
	33	12.8	71.1	17	21	AAAF05272	Hammerhead ribozym
	34	12.8	71.1	17	23	ABK00045	Human NOGO Hamme
	35	12.8	71.1	17	23	ABK00894	Human NOGO Inozyme
	36	12.8	71.1	17	24	AAAL43484	Human tissue kall
	37	12.8	71.1	18	18	AAT95456	Primer for breast
	38	12.8	71.1	18	22	AAH49336	C. glutamicum ATCC
	39	12.8	71.1	20	21	AAZ37997	Human GLCIA gene e
	40	12.8	71.1	20	22	AAAD12118	Rat PTP1B antisens
	41	12.8	71.1	20	24	ABK85193	Rat PTP1B antisens
	42	12.8	71.1	20	24	ABK37362	Rat PTP1B antisens
	43	12.8	71.1	21	18	AAV04186	Primer used when o
	44	12.8	71.1	21	21	AAH47231	Primer 1 for human
	45	12.8	71.1	22	24	AAAD45780	Human promoter -14

ALIGNMENTS

RESULT 1

AAT36243
ID AAT36243 standard; DNA; 18 BP.

AC AAT36243;

XX 25-MAR-2003 (updated)

DT 16-APR-1997 (first entry)

DE CD28 expression inhibiting oligonucleotide, RT09s.

XX Reduction; T cell; CD28; gene expression; treatment; immune system;
XX disorder; graft versus host disease; septic shock; viral disease;
XX psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;
XX multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2;
XX systemic lupus erythematosus; inflammatory bowel disease;
XX IL-2; production; antisense; inhibition; ss

OS Synthetic.

XX WO9624380-A1.

XX 15-AUG-1996.

XX 05-FEB-1996; 96WO-US01507.

XX 09-FEB-1995; 95US-0387041.

XX 18-SEP-1995; 95US-0529878.

XX 09-FEB-1995; 95US-0387041.

XX 18-SEP-1995; 95US-0529878.

PA (ICNC) ICN PHARM INC.
 XX Tam RC;
 XX WPI; 1996-384228/38.
 XX Oligo:nucleotide which reduces CD28 gene expression in T cells -
 PT for treating immune system diseases, e.g. Graft vs. host disease,
 PT septic shock, psoriasis, etc.
 XX
 PS Example 2; Page 45; 77pp; English.
 XX
 CC The present oligonucleotide reduces CD28 dependent interleukin-2
 CC (IL-2) production and T cell CD28 gene expression, useful in the
 CC treatment of CD28 mediated diseases, particularly immune system
 CC disorders, e.g. Graft versus host disease, septic shock, viral
 CC disease, psoriasis, type I diabetes mellitus, thyroiditis,
 CC sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis,
 CC systemic lupus erythematosus, inflammatory bowel disease, etc..
 CC Reducing CD28 expression may reduce the effects of antigenic
 CC stimulation of CD28 positive T cells, with a consequent reduction
 CC in cytokine release.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 18 BP; 2 A; 0 C; 13 G; 3 T; 0 other;
 Query Match 100.0%; Score 18; DB 17; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTGGAGGGGAGGTGGGG 18
 Db 1 TTGGAGGGGAGGTGGGG 18
 RESULT 2
 ID AAX90336 standard; DNA; 18 BP.
 XX
 AC AAX90336;
 XX
 DT 24-SEP-1999 (first entry)
 XX
 DE CD28 inhibiting phosphorothioate oligonucleotide RT09S.
 XX
 KW CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
 KW immune system mediated disease; gamma-interferon; IL-8;
 KW phosphorothioate; ss.
 XX
 OS Synthetic.
 XX
 PN US5932556-A.
 XX
 PD 03-AUG-1999.
 XX
 PF 18-SEP-1995; 95US-0529878.
 XX
 PR 18-SEP-1995; 95US-0529878.
 XX
 PA (TAMR/) TAM R C.
 XX
 PI Tam RC;
 XX
 DR WPI; 1999-443609/37.
 XX
 XX Treatment of immune system-mediated diseases by inhibiting
 PT expression of CD28, IL-2, gamma-interferon or IL-8
 XX
 PS Example; Column 24; 45pp; English.
 XX
 CC The present invention describes a method for inhibiting the expression
 CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
 CC comprises subcutaneous administration of an oligonucleotide (OGN).

CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
 CC method. The OGNs are used for the treatment of immune system-mediated
 CC diseases. The present sequence represents a CD28 inhibiting
 CC phosphorothioate oligonucleotide used in the exemplification of the
 CC present invention.
 XX
 SQ Sequence 18 BP; 2 A; 0 C; 13 G; 3 T; 0 other;
 Query Match 100.0%; Score 18; DB 20; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTGGAGGGGAGGTGGGG 18
 Db 1 TTGGAGGGGAGGTGGGG 18
 RESULT 3
 ID AAT36242 standard; DNA; 18 BP.
 XX
 AC AAT36242;
 XX
 DT 25-MAR-2003 (updated)
 DT 16-APR-1997 (first entry)
 XX
 XX CD28 expression inhibiting oligonucleotide, RT05s.
 DE Reduction; T cell; CD28; gene expression; treatment; immune system;
 XX disorder; graft versus host disease; septic shock; viral disease;
 KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;
 KW multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2;
 KW systemic lupus erythematosus; inflammatory bowel disease;
 KW IL-2; production; antisense; inhibition; ss
 XX
 OS Synthetic.
 XX
 PN WO9624380-A1.
 XX
 PD 15-AUG-1996.
 XX
 PF 05-FEB-1996; 96WO-US01507.
 XX
 PR 09-FEB-1995; 95US-0387041.
 PR 18-SEP-1995; 95US-0529878.
 PR 09-FEB-1995; 95US-0387041.
 PR 18-SEP-1995; 95US-0529878.
 XX
 PA (ICNC) ICN PHARM INC.
 XX
 PI Tam RC;
 XX
 DR WPI; 1996-384228/38.
 XX
 PT Oligo:nucleotide which reduces CD28 gene expression in T cells -
 PT for treating immune system diseases, e.g. Graft vs. host disease,
 PT septic shock, psoriasis, etc.
 XX
 PS Example 2; Page 45; 77pp; English.
 XX
 CC The present oligonucleotide reduces CD28 dependent interleukin-2
 CC (IL-2) production and T cell CD28 gene expression, useful in the
 CC treatment of CD28 mediated diseases, particularly immune system
 CC disorders, e.g. Graft versus host disease, septic shock, viral
 CC disease, psoriasis, type I diabetes mellitus, thyroiditis,
 CC sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis,
 CC systemic lupus erythematosus, inflammatory bowel disease, etc..
 CC Reducing CD28 expression may reduce the effects of antigenic
 CC stimulation of CD28 positive T cells, with a consequent reduction
 CC in cytokine release.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 18 BP; 3 A; 0 C; 13 G; 2 T; 0 other;

Query Match 91.1%; Score 16.4; DB 17; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.4e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGAGGGGAGGTGGGG 18
 DB 1 TTGGAGGGGAGGTGGGG 18

RESULT 4

AAT36196
 ID AAT36196 standard; DNA; 18 BP.

XX
 AC AAT36196;

XX 25-MAR-2003 (updated)

DT 15-APR-1997 (first entry)

XX
 DE Triplex forming oligo targeting CD28 5'-UTR (nt 58-75).

XX Reduction; T cell; CD28; gene expression; treatment; immune system;
 KW disorder; graft versus host disease; septic shock; viral disease;
 KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;
 KW multiple sclerosis; uveitis; rheumatoid arthritis; 5'-UTR;
 KW systemic lupus erythematosus; inflammatory bowel disease;
 KW triplex forming; oligonucleotide; 5'-untranslated region; ss
 XX
 OS Synthetic.

XX
 PN WO9624380-A1.

XX PD 15-AUG-1996.

XX PF 05-FEB-1996; 96WO-US01507.

XX PR 09-FEB-1995; 95US-0387041.

XX PR 18-SEP-1995; 95US-0529878.

XX PR 09-FEB-1995; 95US-0387041.

XX PR 18-SEP-1995; 95US-0529878.

XX PA (ICNC) ICN PHARM INC.

XX PI Tam RC;

XX DR WPI; 1996-384228/38.

XX Oligo:nucleotide which reduces CD28 gene expression in T cells -
 PT for treating immune system diseases, e.g. graft vs. host disease,
 PT septic shock, psoriasis, etc.

XX PS Claim 9; Page 54; 77pp; English.

XX The present oligonucleotide reduces T cell CD28 gene expression,
 CC useful in the treatment of CD28 mediated diseases, particularly
 CC immune system disorders, e.g. graft versus host disease, septic
 CC shock, viral disease, psoriasis; type I diabetes mellitus,
 CC thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid
 CC arthritis, systemic lupus erythematosus, inflammatory bowel
 CC disease, etc.. Reducing CD28 expression may reduce the effects of
 CC antigenic stimulation of CD28 positive T cells, with a consequent
 CC reduction in cytokine release.
 CC (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;

Query Match 91.1%; Score 16.4; DB 17; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.4e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGAGGGGAGGTGGGG 18
 DB 1 TTGGAGGGGAGGTGGGG 18

RESULT 5

AAX90328
 ID AAX90328 standard; DNA; 18 BP.

XX
 AC AAX90328;

XX DT 24-SEP-1999 (first entry)

XX CD28 inhibiting phosphorothioate oligonucleotide RT03S.

XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
 KW immune system mediated disease; gamma-interferon; IL-8;
 KW phosphorothioate; ss.

XX OS Synthetic.

XX PN US5932556-A.

XX PD 03-AUG-1999.

XX PF 18-SEP-1995; 95US-0529878.

XX PR 18-SEP-1995; 95US-0529878.

XX PA (TAMR/) TAM R C.

XX PI Tam RC;

XX DR WPI; 1999-443609/37.

XX Treatment of immune system-mediated diseases by inhibiting
 PT expression of CD28, IL-2, gamma-interferon or IL-8

XX PS Example; Column 21; 45pp; English.

XX CC The present invention describes a method for inhibiting the expression
 CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
 CC comprises subcutaneous administration of an oligonucleotide (OGN).
 CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
 CC method. The OGNs are used for the treatment of immune system-mediated
 CC diseases. The present sequence represents a CD28 inhibiting
 CC phosphorothioate oligonucleotide used in the exemplification of the
 CC present invention.

XX Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;

Query Match 91.1%; Score 16.4; DB 20; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.4e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGAGGGGAGGTGGGG 18
 DB 1 TTGGAGGGGAGGTGGGG 18

RESULT 6

AAX90335
 ID AAX90335 standard; DNA; 18 BP.

XX
 AC AAX90335;

XX DT 24-SEP-1999 (first entry)

XX CD28 inhibiting phosphorothioate oligonucleotide RT05S.

XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
 KW immune system mediated disease; gamma-interferon; IL-8;
 KW phosphorothioate; ss.

XX OS Synthetic.

PN US5932556-A.
 XX 03-AUG-1999.
 PD
 XX
 PF 18-SEP-1995; 95US-0529878.
 XX
 PR 18-SEP-1995; 95US-0529878.
 XX
 PA (TAMR/) TAM R C.
 XX
 PI Tam RC;
 XX
 XX WPI; 1999-443609/37.
 XX
 PT Treatment of immune system-mediated diseases by inhibiting
 expression of CD28, IL-2, gamma-interferon or IL-8
 XX
 XX Example; Column 24; 45pp; English.
 XX
 CC The present invention describes a method for inhibiting the expression
 of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
 comprises subcutaneous administration of an oligonucleotide (OGN).
 CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
 CC method. The OGNs are used for the treatment of immune system-mediated
 CC diseases. The present sequence represents a CD28 inhibiting
 CC phosphorothioate oligonucleotide used in the exemplification of the
 CC present invention.
 XX
 SQ Sequence 18 BP; 3 A; 0 C; 13 G; 2 T; 0 Other;
 Query Match 91.1%; Score 16.4; DB 20; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.4e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 QY 1 TTGGAGGGGAGGTGGG 18
 Db 1 TTGGAGGGGAGGTGGG 18
 XX
 RESULT 7
 AAX90290
 ID AAX90290 standard; DNA; 18 BP.
 XX
 AC AAX90290;
 XX
 DT 24-SEP-1999 (first entry)
 XX
 DE CD28 inhibition oligonucleotide RT03.
 XX
 KW CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
 immune system mediated disease; gamma-interferon; IL-8; ss.
 XX
 OS Synthetic.
 XX
 XX US5932556-A.
 PN
 XX
 PD 03-AUG-1999.
 XX
 PF 18-SEP-1995; 95US-0529878.
 XX
 PR 18-SEP-1995; 95US-0529878.
 XX
 XX (TAMR/) TAM R C.
 PA
 PI Tam RC;
 XX
 XX WPI; 1999-443609/37.
 XX
 PT Treatment of immune system-mediated diseases by inhibiting
 expression of CD28, IL-2, gamma-interferon or IL-8
 XX
 XX Claim 5; Column 29; 45pp; English.

CC The present invention describes a method for inhibiting the expression
 of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
 comprises subcutaneous administration of an oligonucleotide (OGN).
 CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
 CC method. The OGNs are used for the treatment of immune system-mediated
 CC diseases.
 XX
 SQ Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 Other;
 Query Match 91.1%; Score 16.4; DB 20; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.4e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 QY 1 TTGGAGGGGAGGTGGG 18
 Db 1 TTGGAGGGGAGGTGGG 18
 XX
 RESULT 8
 AAX99625
 ID AAX99625 standard; DNA; 18 BP.
 XX
 AC AAX99625;
 XX
 DT 12-JUL-2000 (first entry)
 XX
 DE Nucleotide sequence of G-motif oligonucleotide GR1.
 XX
 KW G-motif oligonucleotide; vaccine; Toxoplasmosis; viral infection;
 antigen presenting cell activation; natural killer cell; septic shock;
 cytotoxic T-lymphocyte; inflammation; autoimmune disease;
 KW rheumatoid arthritis; Crohn's disease; sarcoidosis; multiple sclerosis;
 Kawasaki syndrome; graft-versus-host disease; transplant rejection;
 KW helper T cell response 1-mediated disease; Lyme arthritis;
 KW Streptococcal induced arthritis; chronic inflammatory bowel disease;
 KW psoriasis vulgaris; experimental allergic encephalomyelitis;
 KW insulin-dependent diabetes mellitus; bacterial infection;
 KW parasitic infection; Leishmaniasis; spontaneous abortion; tumour; ss.
 XX
 OS Synthetic.
 XX
 XX WO200014217-A2.
 PN
 XX
 PD 16-MAR-2000.
 XX
 PF 03-SEP-1999; 99WO-EP06502.
 XX
 PR 03-SEP-1998; 98EP-0116652.
 XX
 XX (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.
 PA
 PI Wagner H, Lipford GB, Heeg K;
 XX
 XX WPI; 2000-256970/22.
 DR
 XX
 XX Compositions comprising G-motif oligonucleotides useful for treating
 e.g. septic shock, rheumatoid arthritis, diabetes and human
 PT immunodeficiency virus infections -
 XX
 XX Example 14; Page 32; 75pp; English.
 PS
 XX
 CC The present sequence represents a G-motif oligonucleotide of the
 invention. The specification describes compositions comprising G-motif
 CC oligonucleotides. The G-motif oligonucleotides inhibit activation of
 CC antigen presenting cells by inhibiting the uptake of DNA by a cell, by
 CC stimulating natural killer cells, or by co-stimulating cytotoxic
 CC T-lymphocytes. The G-motif oligonucleotides may be used for the
 CC production of vaccines for treating septic shock, inflammation,
 CC autoimmune diseases (e.g. rheumatoid arthritis, Crohn's disease,
 CC sarcoidosis, multiple sclerosis, Kawasaki syndrome, graft-versus-host
 CC disease and transplant rejection), helper T cell response 1-mediated
 CC diseases (e.g. Streptococcal induced arthritis, Lyme arthritis, chronic
 CC inflammatory bowel disease, psoriasis vulgaris, experimental allergic

CC encephalomyelitis, and insulin-dependent diabetes mellitus), bacterial
 CC infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis),
 CC viral infections (e.g. Cytomegalovirus and human immunodeficiency virus
 CC (HIV)-infections), spontaneous abortions and tumours. They may also be
 CC used to induce proliferation of bone marrow cells, especially macrophage
 CC precursor cells.

XX Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;
 SQ Query Match 91.1%; Score 16.4; DB 21; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.4e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 TTGAGGGGGAGGTGGG 18
 |||||
 Db 1 TTGAGGGGGTGTGGG 18

RESULT 9
 AAZ99650/C
 ID AAZ99650 standard; DNA; 18 BP.
 XX AC
 XX AAZ99650;
 DT 12-JUL-2000 (first entry)
 XX DE Nucleotide sequence of non-G-motif oligonucleotide GRP1comp.
 XX KW G-motif oligonucleotide; vaccine; Toxoplasmosis; viral infection;
 KW antigen presenting cell activation; natural killer cell; septic shock;
 KW cytotoxic T-lymphocyte; inflammation; autoimmune disease;
 KW rheumatoid arthritis; Crohn's disease; sarcoidosis; multiple sclerosis;
 KW Kawasaki syndrome; graft-versus-host disease; transplant rejection;
 KW helper T cell response 1-mediated disease; Lyme arthritis;
 KW Streptococcal induced arthritis; chronic inflammatory bowel disease;
 KW psoriasis vulgaris; experimental allergic encephalomyelitis;
 KW insulin-dependent diabetes mellitus; bacterial infection;
 KW parasitic infection; Leishmaniasis; spontaneous abortion; tumour; ss.
 XX OS Synthetic.

XX WO200014217-A2.
 PN 16-MAR-2000.
 PD 03-SEP-1999; 99WO-EP06502.
 PF 03-SEP-1999; 98EP-0116652.
 PR (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.
 XX PA
 XX Wagner H, Lipford GB, Heeg K;
 PI WPI; 2000-256970/22.
 XX DR
 XX Compositions comprising G-motif oligonucleotides useful for treating
 PT e.g. septic shock, rheumatoid arthritis, diabetes and human
 PT immunodeficiency virus infections -
 XX Example 14; Page 32; 75pp; English.

XX The present sequence represents a non-G-motif oligonucleotide of the
 CC invention. The specification describes compositions comprising G-motif
 CC oligonucleotides. The G-motif oligonucleotides inhibit activation of
 CC antigen presenting cells by inhibiting the uptake of DNA by a cell, by
 CC stimulating natural killer cells, or by co-stimulating cytotoxic
 CC T-lymphocytes. The G-motif oligonucleotides may be used for the
 CC productions of vaccines for treating septic shock, inflammation,
 CC autoimmune diseases (e.g. rheumatoid arthritis, Crohn's disease,
 CC sarcoidosis, multiple sclerosis, Kawasaki syndrome, graft-versus-host
 CC disease and transplant rejection), helper T cell response 1-mediated
 CC diseases (e.g. Streptococcal induced arthritis, Lyme arthritis, chronic
 CC inflammatory bowel disease, psoriasis vulgaris, experimental allergic

CC encephalomyelitis, and insulin-dependent diabetes mellitus), bacterial
 CC infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis),
 CC viral infections (e.g. Cytomegalovirus and human immunodeficiency virus
 CC (HIV)-infections), spontaneous abortions and tumours. They may also be
 CC used to induce proliferation of bone marrow cells, especially macrophage
 CC precursor cells.

XX Sequence 18 BP; 4 A; 13 C; 0 G; 1 T; 0 other;
 SQ Query Match 91.1%; Score 16.4; DB 21; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.4e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 TTGAGGGGGAGGTGGG 18
 |||||
 Db 18 TTGAGGGGGTGTGGG 1

RESULT 10
 AAT36197
 ID AAT36197 standard; DNA; 21 BP.
 XX AC
 XX AAT36197;
 DT 25-MAR-2003 (updated)
 DT 15-APR-1997 (first entry)
 XX DE Triplex forming oligo targeting CD28 5'-UTR (nt 58-78).
 XX KW Reduction; T cell; CD28; Gene expression; treatment; immune system;
 KW disorder; graft versus host disease; septic shock; viral disease;
 KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;
 KW multiple sclerosis; uveitis; rheumatoid arthritis; 5'-UTR;
 KW systemic lupus erythematosus; inflammatory bowel disease;
 KW triplex forming; oligonucleotide; 5'-untranslated region; ss
 XX OS Synthetic.
 XX WO9624380-A1.
 XX 15-AUG-1996.
 XX 05-FEB-1996; 96WO-US01507.
 XX 09-FEB-1995; 95US-0387041.
 PR 18-SEP-1995; 95US-0529878.
 PR 09-FEB-1995; 95US-0387041.
 PR 18-SEP-1995; 95US-0529878.
 XX (ICNC) ICN PHARM INC.
 XX Tam RC;
 XX WPI; 1996-384228/38.
 XX Oligo:nucleotide which reduces CD28 gene expression in T cells -
 PT for treating immune system diseases, e.g. graft vs. host disease,
 PT septic shock, psoriasis, etc.
 XX Claim 10; Page 54; 77pp; English.

XX The present oligonucleotide reduces T cell CD28 gene expression,
 CC useful in the treatment of CD28 mediated diseases, particularly
 CC immune system disorders, e.g. graft versus host disease, septic
 CC shock, viral disease, psoriasis, type I diabetes mellitus,
 CC thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid
 CC arthritis, systemic lupus erythematosus, inflammatory bowel
 CC disease, etc.. Reducing CD28 expression may reduce the effects of
 CC antigenic stimulation of CD28 positive T cells, with a consequent
 CC reduction in cytokine release.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;

Query Match 91.1%; Score 16.4; DB 17; Length 21;
 Best Local Similarity 94.4%; Pred. No. 1.4e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TTGGAGGGGAGGTGGGG 18
 DB 4 TTGGAGGGGAGGTGGGG 21

RESULT 11
 AAX90329
 ID AAX90329 standard; DNA; 21 BP.
 XX
 AC AAX90329;
 XX
 DT 24-SEP-1999 (first entry)
 XX
 DE CD28 inhibiting phosphorothioate oligonucleotide RT04S.
 XX
 XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
 KW immune system mediated disease; gamma-interferon; IL-8;
 KW phosphorothioate; ss.
 XX
 OS Synthetic.
 XX US5932556-A.
 PN 03-AUG-1999.
 PD 18-SEP-1995; 95US-0529878.
 PF 18-SEP-1995; 95US-0529878.
 PP 18-SEP-1995; 95US-0529878.
 PR (TAMR/) TAM R C.
 PA Tam RC;
 PI WPI; 1999-443609/37.
 DR
 XX Treatment of immune system-mediated diseases by inhibiting
 PT expression of CD28, IL-2, gamma-interferon or IL-8
 PT
 XX Claim 6; Column 29; 45pp; English.

XX The present invention describes a method for inhibiting the expression
 CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
 CC comprises subcutaneous administration of an oligonucleotide (OGN).
 CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
 CC method. The OGNs are used for the treatment of immune system-mediated
 CC diseases. The present sequence represents a CD28 inhibiting
 CC phosphorothioate oligonucleotide used in the exemplification of the
 CC present invention.
 XX
 SQ Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;
 Query Match 91.1%; Score 16.4; DB 20; Length 21;
 Best Local Similarity 94.4%; Pred. No. 1.4e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TTGGAGGGGAGGTGGGG 18
 DB 4 TTGGAGGGGAGGTGGGG 21

RESULT 12
 AAX90291
 ID AAX90291 standard; DNA; 21 BP.
 XX
 AC AAX90291;
 XX
 DT 24-SEP-1999 (first entry)
 XX
 DE CD28 inhibiting phosphorothioate oligonucleotide RT04S.
 XX
 XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
 KW immune system mediated disease; gamma-interferon; IL-8;
 KW phosphorothioate; ss.
 XX
 OS Synthetic.
 XX US5932556-A.
 PN 03-AUG-1999.
 PD 18-SEP-1995; 95US-0529878.
 PF 18-SEP-1995; 95US-0529878.
 PP 18-SEP-1995; 95US-0529878.
 PR (TAMR/) TAM R C.
 PA Tam RC;
 PI WPI; 1999-443609/37.
 DR
 XX Treatment of immune system-mediated diseases by inhibiting
 PT expression of CD28, IL-2, gamma-interferon or IL-8
 PT
 XX Claim 6; Column 21; 45pp; English.

XX The present invention describes a method for inhibiting the expression
 CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
 CC comprises subcutaneous administration of an oligonucleotide (OGN).
 CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
 CC method. The OGNs are used for the treatment of immune system-mediated
 CC diseases. The present sequence represents a CD28 inhibiting
 CC phosphorothioate oligonucleotide used in the exemplification of the
 CC present invention.
 XX
 SQ Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;
 Query Match 91.1%; Score 16.4; DB 20; Length 21;
 Best Local Similarity 94.4%; Pred. No. 1.4e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TTGGAGGGGAGGTGGGG 18
 DB 4 TTGGAGGGGAGGTGGGG 21

RESULT 13
 AAF16593
 ID AAF16593 standard; DNA; 22 BP.
 XX
 AC AAF16593;
 XX
 DT 13-MAR-2001 (first entry)
 XX
 DE Gastric acid production inhibiting oligonucleotide SEQ ID NO: 79.
 XX
 KW Gastric acid disturbance; gastric reflux; gastritis; dyspepsia;
 KW stomach ulcer; duodenal ulcer; Helicobacter pylori; antisense;
 KW DNA-RNA hybrid; ss.
 XX
 OS Synthetic.
 XX WO2000071164-A1.
 PN 30-NOV-2000.
 PD 24-MAY-2000; 2000WO-AU00498.
 PP 24-MAY-1999; 99AU-0000510.
 PR (TACH/) TACHAS G.
 PA Tachas G;
 PI WPI; 2001-025093/03.
 DR

DE CD28 inhibition oligonucleotide RT04.
 XX
 KW CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
 KW immune system mediated disease; gamma-interferon; IL-8; ss.
 XX
 OS Synthetic.
 XX US5932556-A.
 PN 03-AUG-1999.
 PD 18-SEP-1995; 95US-0529878.
 PF 18-SEP-1995; 95US-0529878.
 PP 18-SEP-1995; 95US-0529878.
 PR (TAMR/) TAM R C.
 PA Tam RC;
 PI WPI; 1999-443609/37.
 DR
 XX Treatment of immune system-mediated diseases by inhibiting
 PT expression of CD28, IL-2, gamma-interferon or IL-8
 PT
 XX Claim 6; Column 29; 45pp; English.

XX The present invention describes a method for inhibiting the expression
 CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
 CC comprises subcutaneous administration of an oligonucleotide (OGN).
 CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
 CC method. The OGNs are used for the treatment of immune system-mediated
 CC diseases.
 XX
 SQ Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;
 Query Match 91.1%; Score 16.4; DB 20; Length 21;
 Best Local Similarity 94.4%; Pred. No. 1.4e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TTGGAGGGGAGGTGGGG 18
 DB 4 TTGGAGGGGAGGTGGGG 21

XX Treating gastric acid disturbance by administering an oligonucleotide
 PT which modulates the activity of a polypeptide involved in gastric acid
 PT production or secretion -
 XX Example 3; Page 145; 164pp; English.
 XX The present invention provides oligonucleotides, and methods for their
 CC use, which are useful in modulating the action of proteins involved in
 CC gastric acid production. The target protein is preferably the histamine
 CC H2 receptor or one of the proteins which form part of the gastric proton
 CC pump. The sequences and methods of the invention are useful in the
 CC treatment of gastric reflux, gastritis, dyspepsia, stomach ulcers,
 CC duodenal ulcers and other gastric acid disturbances, most of which are
 CC caused by *Helicobacter pylori*.
 XX Sequence 22 BP; 0 A; 0 C; 16 G; 3 T; 3 other;

Query Match 82.2%; Score 14.8; DB 22; Length 22;
 Best Local Similarity 81.2%; Pred. No. 5.8e+03;
 Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGAGGGGAGGTGGG 17
 DB 2 TGGAGGGGAGGTGGG 17

RESULT 14
 AAF01954/c
 ID AAF01954 standard; DNA; 17 BP.

XX AAF01954;

DT 16-FEB-2001 (first entry)

DE Hammerhead ribozyme substrate #249.

XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.

XX Homo sapiens.

XX WO200061729-A2.

XX 19-OCT-2000.

XX 11-APR-2000; 2000WO-US09721.

XX 12-APR-1999; 99US-0129390.

XX (RIBO-) RIBOZYME PHARM INC.

PI Blatt L, Zwick M, Pavco P, McSwiggen J;

XX WPI; 2000-647423/62.

XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
 PT useful for producing e.g. granulocyte colony stimulating factor
 PT protein, interferon alpha and erythropoietin -

PS Claim 37; Page 61; 164pp; English.

XX The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
 CC transcription factor gene, IRF-2 and/or the C/EBP Displacement
 CC Protein (CDP). Inhibition of the repressors removes prevents
 CC inhibition (and consequently increases expression of) genes involved in
 CC the production of erythropoietin, granulocyte colony stimulating factor
 CC protein and interferon alpha.

XX Sequence 17 BP; 2 A; 12 C; 0 G; 3 T; 0 other;

Query Match 80.0%; Score 14.4; DB 21; Length 17;
 Best Local Similarity 93.8%; Pred. No. 8.4e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGGGAGGTGGG 18
 DB 16 GGAGGGGAGGTGGG 1

RESULT 15

AA012117
 ID AAD12117 standard; DNA; 20 BP.

XX AAD12117;

XX 25-SEP-2001 (first entry)

XX Rat PTP1B antisense oligonucleotide (ISIS# 113721).

XX Rat; PTP1B; protein phosphatase 1B inhibitor; antisense; gene therapy;
 KW infection; inflammation; tumour; prophylaxis; phosphorothioate; ss.

XX *Rattus norvegicus*.

XX Synthetic.

XX Key Location/Qualifiers

FT modified_base 1..20

FT /tag= a

FT /mod_base= OTHER

FT /note= "Phosphorothioate backbone"

FT modified_base 1..5

FT /tag= b

FT /mod_base= OTHER

FT /note= "Methoxyethyl residues"

FT modified_base 16..20

FT /tag= c

FT /mod_base= OTHER

FT /note= "Methoxyethyl residues"

FT modified_base 4..5

FT /tag= d

FT /mod_base= m5c

FT modified_base 19

FT /tag= e

FT /mod_base= m5c

XX US6261840-B1.

XX 17-JUL-2001.

XX 18-JAN-2000; 2000US-0487368.

XX 18-JAN-2000; 2000US-0487368.

XX (ISIS-) ISIS PHARM INC.

XX Cowsert LM, Wyatt J;

XX WPI; 2001-432181/46.

XX New antisense compounds capable of modulating expression of human
 PT protein phosphatase 1B, useful for diagnosis, prophylaxis and treatment
 PT of diseases associated with expression of protein phosphatase -

XX Example 17; Column 51-52; 71pp; English.

XX The invention is directed to antisense compounds, particularly
 CC oligonucleotides which are targeted to a DNA encoding protein
 CC phosphatase 1B (PTP1B) to modulate its expression. The antisense
 CC compounds are useful for diagnosis, prophylaxis and treatment of
 CC diseases associated with the expression of PTP1B, to prevent or
 CC delay infection, inflammation and tumour formation and as a
 CC research reagent. The PTP1B DNA is useful in gene therapy.
 CC The present sequence is an antisense oligonucleotide with a

CC phosphorothioate backbone. This oligo is targeted to rat
CC PTP1B to inhibit its expression.

XX
SQ Sequence 20 BP; 2 A; 3 C; 13 G; 2 T; 0 other;

Query Match 76.7%; Score 13.8; DB 22; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.4e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGAGGGGGAGGTGGGG 18
||| |||||
Db 1 TGGCCGGGGAGGTGGGG 17

Search completed: October 27, 2003, 11:25:21
Job time : 163 secs

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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 11:09:34 ; Search time 307.029 Seconds
(without alignments)
97.777 Million cell updates/sec

Title: US-09-331-204A-7

Perfect score: 18

Sequence: 1 ttggaggggaggaagggg 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2231628 seqs, 833900706 residues

Total number of hits satisfying chosen parameters: 264402

Minimum DB seq length: 0

Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents NA New:*

- 1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
- 2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
- 3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
- 4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
- 5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
- 6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
- 7: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	94.4	19	1	PCT-US02-38216-47426
2	15	83.3	18	1	PCT-US02-38216-6227
3	14.8	82.2	22	1	PCT-US02-38216-18159
4	14.4	80.0	16	1	PCT-US02-38216-39032
5	14.4	80.0	17	1	PCT-US02-38216-38911
6	14.4	80.0	18	1	PCT-US02-38216-6229
7	14.4	80.0	18	1	PCT-US02-38216-39031
8	14.4	80.0	18	1	PCT-US02-38216-41647
9	14.4	80.0	19	1	PCT-US02-38216-38912
10	14.4	80.0	21	1	PCT-US03-11936A-126
11	14	77.8	17	1	PCT-US02-38216-6220
12	14	77.8	17	1	PCT-US02-38216-38954
13	14	77.8	19	1	PCT-US02-38216-26652
14	13.8	76.7	17	1	PCT-US02-38216-18314
15	13.8	76.7	18	1	PCT-US02-38216-14763
16	13.8	76.7	19	1	PCT-US02-38216-18278
17	13.8	76.7	22	1	PCT-US02-38216-58271
18	13.4	74.4	16	1	PCT-US02-38216-39060
19	13.4	74.4	16	1	PCT-US02-38216-60967
20	13.4	74.4	16	1	PCT-US02-38216-61070
21	13.4	74.4	17	1	PCT-US02-38216-5920
22	13.4	74.4	17	1	PCT-US02-38216-18251
23	13.4	74.4	17	1	PCT-US02-38216-38987
24	13.4	74.4	17	1	PCT-US02-38216-48877
25	13.4	74.4	17	1	PCT-US02-38216-58278
26	13.4	74.4	17	1	PCT-US02-38216-58297

27	13.4	74.4	17	1	PCT-US02-38216-60884	Sequence 60884, A
28	13.4	74.4	18	1	PCT-US02-38216-18290	Sequence 18290, A
29	13.4	74.4	18	1	PCT-US02-38216-25803	Sequence 25803, A
30	13.4	74.4	18	1	PCT-US02-38216-38927	Sequence 38927, A
31	13.4	74.4	18	1	PCT-US02-38216-39001	Sequence 39001, A
32	13.4	74.4	18	1	PCT-US02-38216-39023	Sequence 39023, A
33	13.4	74.4	18	1	PCT-US02-38216-41601	Sequence 41601, A
34	13.4	74.4	19	1	PCT-US02-38216-6296	Sequence 6296, Ap
35	13.4	74.4	19	1	PCT-US02-38216-26644	Sequence 26644, A
36	13.4	74.4	19	1	PCT-US02-38216-38922	Sequence 38922, A
37	13.4	74.4	19	1	PCT-US02-38216-60003	Sequence 60003, A
38	13.4	74.4	20	1	PCT-US02-38216-39088	Sequence 39088, A
39	13.4	74.4	20	1	PCT-US02-38216-52911	Sequence 52911, A
40	13.4	74.4	21	1	PCT-US02-38216-38986	Sequence 38986, A
41	13.4	74.4	22	1	PCT-US02-38216-27400	Sequence 27400, A
42	13.2	73.3	18	1	PCT-US02-38216-18060	Sequence 18060, A
43	13.2	73.3	20	1	PCT-US02-38216-992	Sequence 992, App
44	13.2	73.3	22	1	PCT-US02-38216-26562	Sequence 26562, A
45	13	72.2	15	1	PCT-US02-38216-61080	Sequence 61080, A

ALIGNMENTS

RESULT 1
PCT-US02-38216-47426
; Sequence 47426, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICAALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 47426
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-47426

Query Match 94.4%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGGAGGGGGAGGAGGGG 18
Db 3 TGGAGGGGGAGGAGGGG 19

RESULT 2
PCT-US02-38216-6227/c
; Sequence 6227, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICAALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 6227
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-6227

Query Match 83.3%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGAGGG 17
Db 15 GGAGGGGGAGGAGGG 1

RESULT 3
PCT-US02-38216-18159
; Sequence 18159, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 18159
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-18159

Query Match 82.2%; Score 14.8; DB 1; Length 22;
Best Local Similarity 88.9%; Pred. No. 1.1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGAGGAGGG 18
Db 1 TGGAGGGGGAGGAGGG 18

RESULT 4
PCT-US02-38216-39032
; Sequence 39032, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 39032
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-39032

Query Match 80.0%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGAGGG 18
Db 1 GGAGGGGGAGGAGGG 16

RESULT 5
PCT-US02-38216-38911
; Sequence 38911, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 38911
; LENGTH: 17

; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-38911

Query Match 80.0%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGAGGG 18
Db 1 GGAGGGGGAGGAGGG 16

RESULT 6
PCT-US02-38216-6229/c
; Sequence 6229, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 6229
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-6229

Query Match 80.0%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGAGGG 18
Db 16 GGAAGGGGGAGGAGGG 1

RESULT 7
PCT-US02-38216-39031
; Sequence 39031, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 39031
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-39031

Query Match 80.0%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGAGGG 18
Db 3 GGAGGGGGAGGAGGG 18

RESULT 8
PCT-US02-38216-41647
; Sequence 41647, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY

; TITLE OF INVENTION: GENES AND USES THEREOF
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41647
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-41647

Query Match 80.0%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGAGGGG 18
| | | | | | | | | | | | | | | | | |
Db 1 GGAGGGGGTGGAGGGG 16

RESULT 9
PCT-US02-38216-38912
; Sequence 38912, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38912
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-38912

Query Match 80.0%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGAGGGG 18
| | | | | | | | | | | | | | | | | |
Db 3 GGAGGGAGGAGGAGGGG 18

RESULT 10
PCT-US03-11936A-126/c
; Sequence 126, Application PC/TUS0311936A
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; TITLE OF INVENTION: UNIVERSAL LIBRARIES FOR IMMUNOGLOBULINS
; FILE REFERENCE: 1551.2001003
; CURRENT APPLICATION NUMBER: PCT/US03/11936A
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/373,558
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 423
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
PCT-US03-11936A-126

Query Match 80.0%; Score 14.4; DB 1; Length 21;
Best Local Similarity 93.8%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGAGGGG 18
| | | | | | | | | | | | | | | | | |
Db 17 GGAGGGGGAGGAGGAG 2
| | | | | | | | | | | | | | | | | |
RESULT 11
PCT-US02-38216-6220/c
; Sequence 6220, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6220
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-6220

Query Match 77.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGAGG 16
| | | | | | | | | | | | | | | |
Db 14 GGAGGGGGAGGAGG 1

RESULT 12
PCT-US02-38216-38954
; Sequence 38954, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38954
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-38954

Query Match 77.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGGGGAGGAGGG 17
| | | | | | | | | | | | | | | |
Db 2 GAGGGGGAGGAGGG 15

RESULT 13
PCT-US02-38216-26652/c
; Sequence 26652, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26652
; LENGTH: 19

```
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-26652

Query Match      77.8%; Score 14; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGGGGAGGAGGG 18
   |||||
Db 14 AGGGGAGGAGGG 1

RESULT 14
PCT-US02-38216-18314
; Sequence 18314, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18314
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-18314

Query Match      76.7%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.4e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGGAGGGGAGGAGGG 18
   |||||
Db 1 TGGAGGGGAGGAGGG 17

RESULT 15
PCT-US02-38216-14763
; Sequence 14763, Application PC/TUS0238216
; GENERAL INFORMATION:
; APPLICANT: Rosetta Genomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55002
; CURRENT APPLICATION NUMBER: PCT/US02/38216
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14763
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38216-14763

Query Match      76.7%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 2.4e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGGAGGGGAGGAGGG 17
   |||||
Db 1 TGGAGGGGAGGAGGG 17

Search completed: October 27, 2003, 18:22:55
Job time : 307.029 secs
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1978032"
/tissue_type="tumor, 5 pooled (see description)"
/lab_host="DH10B"
/clone_lib="NCI CGAP Brn35"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.33 kb. Tumor types include:
meningioma, oligodendroglioma, astrocytoma (grade II),
medulloblastoma, astrocytoma (grade IV). Life technologies
catalog #: 11544-012"

4 a 14 c 0 g 1 t

BASE COUNT
ORIGIN

Query Match 76.7%; Score 13.8; DB 9; Length 19;
Best Local Similarity 88.2%; Pred. No. 4.8e-05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGGAGGGGAGGAGGG 17
|||||
Db 17 TTGGGGGGGAGGGGG 1

RESULT 2

AZ876923 22 bp DNA linear GSS 21-FEB-2001
LOCUS 2M0192D07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0192D07 F, genomic survey sequence.

ACCESSION AZ876923
VERSION GSS
KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

COMMENT

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0192 Row: D Column: 07

Seq primer: CTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

FEATURES

source

1..22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0192D07"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 4 a 1 c 15 g 2 t

ORIGIN

Query Match 76.7%; Score 13.8; DB 28; Length 22;
Best Local Similarity 88.2%; Pred. No. 4.8e-05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGGAGGGGAGGAGGG 17
|||||
Db 2 TTGGAGGAGGAGGGGG 18

RESULT 3

AU254493

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished

Contact: Kikuya Kato

Graduate School of Biological Sciences

Nara Institute of Science and Technology

8916-5 Takayama, Ikoma, Nara 630-0101, Japan

Tel: 81-743-72-5591

Fax: 81-743-72-5599

Email: kkat@bs.aist-nara.ac.jp

URL: http://love2.aist-nara.ac.jp/BS/index.html.

Location/Qualifiers

1..21

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="BED0002246"

/tissue_type="brain"

/clone_lib="3'-directed mouse cDNA library"

3 a 7 c 14 g 2 t

BASE COUNT

ORIGIN

Query Match 74.4%; Score 13.4; DB 9; Length 21;
Best Local Similarity 93.3%; Pred. No. 6.3e-05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAGGGGAGGAGGGG 18
|||||

Db 7 GTGGGGGAGGAGGGG 21

RESULT 4

AI582080/c

LOCUS

AI582080

22 bp mRNA linear EST 06-APR-1999

84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: G column: 12
Seq primer: CACACAGGAAACAGCTATACCC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES

source

1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0080G12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 1 a 1 c 17 g 0 t
ORIGIN
Query Match 71.1%; Score 12.8; DB 28; Length 19;
Best Local Similarity 87.5%; Pred. No. 9.7e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 GGAGGGGGAGGAGGGG 18
||| ||||| ||||| |||||
Db 2 GGGGGGGAGGAGGGG 17

RESULT 7

AZ447248/c
LOCUS 19 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0244H23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0244H23 F, genomic survey sequence.
ACCESSION AZ447248.1 GI:10599044
VERSION
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0244 row: H column: 23
Seq primer: CGTGTAAACACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES

source

1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0244H23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 18 c 0 g 1 t
ORIGIN
Query Match 71.1%; Score 12.8; DB 28; Length 19;
Best Local Similarity 87.5%; Pred. No. 9.7e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 GGAGGGGGAGGAGGGG 18
||| ||||| ||||| |||||
Db 16 GGGGGGGAGGAGGGG 1

RESULT 8

AZ579189/c
LOCUS 19 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0363I12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0363I12 F, genomic survey sequence.
ACCESSION AZ579189.1 GI:11693534
VERSION
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0363 row: 1 column: 12
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES

source

1. 19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0363112"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 0 a 16 c 0 g 3 t
ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 19;
Best Local Similarity 87.5%; Pred. No. 9.7e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGAGGGG 18
Db 16 GGAGGGGGAGGAGGGG 1

RESULT 9
AZ760597/c 19 bp DNA linear GSS 16-FEB-2001
LOCUS
DEFINITION
1M0554N21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0554N21 F, genomic survey sequence.

ACCESSION
AZ760597
VERSION
AZ760597.1 Gi:12868613
KEYWORDS
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished
Contact: Robert B. Weiss

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0554 row: N column: 21
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES

source

1. 19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0554N21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 0 a 18 c 0 g 1 t
ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 19;
Best Local Similarity 87.5%; Pred. No. 9.7e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGAGGAGGGG 18
Db 18 GGAGGGGGGGGGGGGG 3

RESULT 10

AZ775540

LOCUS

DEFINITION

2M0008H15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0008H15 F, genomic survey sequence.

ACCESSION

AZ775540

VERSION

AZ775540.1 Gi:12902183

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

Unpublished

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0008 row: H column: 15
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES

source

1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M008H15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 7 a 0 c 12 g 0 t

ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 19;
Best Local Similarity 87.5%; Pred. No. 9.7e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGAGGGGAGGAGGGG 18

Db 2 GGAGGGGAGGAGGAG 17

RESULT 11

AZ783420/c

LOCUS

2M0025D07F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGC2M0025D07 F, genomic survey sequence.

ACCESSION

AZ783420

VERSION

AZ783420.1

KEYWORDS

GSS.

SOURCE

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 19)

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly

M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

and Wright, D. Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

TITLE

plasmid inserts

JOURNAL

COMMENT

Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0025 row: D column: 07
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES

source

1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0025D07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 17 c 0 g 2 t

ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 19;
Best Local Similarity 87.5%; Pred. No. 9.7e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGAGGGGAGGAGGGG 18

Db 19 GGGGGGGGGGAGGGG 4

RESULT 12

AZ512326/c

LOCUS

1M0357118R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM0357118 R, genomic survey sequence.

ACCESSION

AZ512326

VERSION

AZ512326.1

KEYWORDS

GSS.

SOURCE

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 20)

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly

M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

and Wright, D. Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

TITLE

plasmid inserts

```

JOURNAL
COMMENT
Plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0357 row: 1 column: 18
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0510B10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      0 a      18 c      0 g      2 t
ORIGIN
Query Match      71.1%; Score 12.8; DB 28; Length 20;
Best Local Similarity 87.5%; Pred. No. 9.7e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 GGAGGGGGAGGAGGGG 18
        |||||||
Db      18 GGAGGGGGGGGGGGGG 3

RESULT 13
AZ645269/c
LOCUS
DEFINITION
clone UUGC1M0510B10 R, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.

Plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0357 row: 1 column: 18
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. .20
/organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      0 a      18 c      0 g      2 t
ORIGIN
Query Match      71.1%; Score 12.8; DB 28; Length 20;
Best Local Similarity 87.5%; Pred. No. 9.7e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 GGAGGGGGAGGAGGGG 18
        |||||||
Db      18 GGAGGGGGGGGGGGGG 3

RESULT 14
AZ659755/c
LOCUS
DEFINITION
clone UUGC1M0537P22 F, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0510 row: B column: 10
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. .20
/organism="Mus musculus"
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/db_xref="taxon:10090"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      0 a      19 c      0 g      1 t
ORIGIN
Query Match      71.1%; Score 12.8; DB 28; Length 20;
Best Local Similarity 87.5%; Pred. No. 9.7e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 GGAGGGGGAGGAGGGG 18
        |||||||
Db      17 GGAGGGGGGGGGGGGG 2

RESULT 14
AZ659755/c
LOCUS
DEFINITION
clone UUGC1M0537P22 F, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.

```

TITLE
 JOURNAL
 COMMENT

and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0537 row: F column: 22
 Seq primer: CCGTGTAAACGACGCCGAGT
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers

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 /organism="Mus musculus"
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 /strain="C57BL/6J"
 /db_xref="taxon:10090"
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 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 0 a 18 c 0 g 2 t

ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 20;
 Best Local Similarity 87.5%; Pred. No. 9.7e+05;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGGAGGAGGGG 18

|||||
 Db 20 GGAGGGGGGAGGAGGGG 5

RESULT 15

AZ772707/c
 LOCUS
 DEFINITION
 1M0583L18R Mouse 10kb plasmid UUC1M library Mus musculus genomic
 clone UUC1M0583L18 R, genomic survey sequence.

ACCESSION AZ772707.1 GI:12896303

VERSION GSS.

KEYWORDS Mus musculus

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE
 AUTHORS
 1 (bases 1 to 20)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0583 row: L column: 18
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers

source

1. ..20
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC1M0583L18"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 0 a 19 c 0 g 1 t

ORIGIN

Query Match 71.1%; Score 12.8; DB 28; Length 20;
 Best Local Similarity 87.5%; Pred. No. 9.7e+05;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGGGAGGAGGGG 18

|||||
 Db 19 GGAGGGGGGAGGAGGGG 4

Search completed: October 27, 2003, 13:59:27

Job time : 1582.77 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:34 ; Search time 41.3143 Seconds
(without alignments)
192.304 Million cell updates/sec

Title: US-09-331-204A-7
Perfect score: 18
Sequence: 1 ttggagggggagggggg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 376294

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15.4	83.6	21	3	US-09-092-077-45
2	14.8	82.2	18	2	US-08-523-878B-3
3	14.8	82.2	18	2	US-08-523-878B-44
4	14.8	82.2	21	2	US-08-523-878B-4
5	14.8	82.2	21	2	US-08-523-878B-45
C	6	14.4	80.0	17	US-08-173-489C-127
7	13.8	76.7	20	4	US-09-780-173A-93
C	8	13.4	74.4	20	US-09-661-753-30
9	12.8	71.1	17	4	US-09-495-140-26
10	12.8	71.1	18	3	US-09-344-579-9
C	11	12.8	71.1	20	US-09-490-652-153
C	12	12.8	71.1	21	US-08-256-426B-282
13	12.8	71.1	21	2	US-08-863-639A-41
C	14	12.8	71.1	21	US-08-863-639A-53
C	15	12.8	71.1	21	US-08-863-639A-59
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17	12.8	71.1	21	2	US-08-863-639A-70
C	18	12.8	71.1	21	US-08-863-639A-83
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C	20	12.8	71.1	21	PCT-US95-07349-5
21	12.4	68.9	22	1	US-08-398-613A-51
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23	12.4	68.9	22	1	US-08-398-612A-51
24	12.4	68.9	22	1	US-08-398-612A-54
25	12.4	68.9	22	1	US-08-398-611A-51
26	12.4	68.9	22	1	US-08-398-611A-54
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28	12.4	68.9	22	1	US-08-396-851A-54	Sequence 54, Appl	
29	12.4	68.9	22	2	US-08-491-334A-51	Sequence 51, Appl	
30	12.4	68.9	22	2	US-08-491-334A-54	Sequence 54, Appl	
31	12.4	68.9	22	3	US-09-027-449-38	Sequence 38, Appl	
32	12.4	68.9	22	3	US-08-804-444A-38	Sequence 38, Appl	
33	12.4	68.9	22	3	US-09-026-985-38	Sequence 38, Appl	
34	12.4	68.9	22	4	US-09-121-952A-38	Sequence 38, Appl	
35	12.4	68.9	22	4	US-09-234-340A-38	Sequence 38, Appl	
C	36	12.4	68.9	22	6	5256545-40	Patent No. 5256545
C	37	12.2	67.8	19	1	US-08-486-913-2	Sequence 2, Appl
C	38	12.2	67.8	19	2	US-08-486-535-2	Sequence 2, Appl
C	39	12.2	67.8	19	2	US-08-300-484-2	Sequence 2, Appl
C	40	12.2	67.8	19	3	US-08-486-885-2	Sequence 2, Appl
C	41	12.2	67.8	19	3	US-08-486-536-2	Sequence 2, Appl
C	42	12.2	67.8	19	5	PCT-US95-11234-2	Sequence 2, Appl
43	12.2	67.8	20	1	US-08-486-913-3	Sequence 3, Appl	
44	12.2	67.8	20	2	US-08-486-535-3	Sequence 3, Appl	
45	12.2	67.8	20	2	US-08-300-484-3	Sequence 3, Appl	

ALIGNMENTS

RESULT 1
US-09-092-077-45
: Sequence 45, Application US/09092077
: Patent No. 6194142
: GENERAL INFORMATION:
: APPLICANT: Moncany, Maurice
: APPLICANT: Montagnier, Luc
: TITLE OF INVENTION: Nucleotide Sequences Derived From The
: TITLE OF INVENTION: Genome Of Retroviruses Of The HIV-1, HIV-2 And SIV Type,
: TITLE OF INVENTION: And Their Uses In Particular For The Amplification Of The
: TITLE OF INVENTION: Genomes Of These Retroviruses And For The In Vitro Diagnosis
: TITLE OF INVENTION: Of The Diseases Due To Those Viruses
: NUMBER OF SEQUENCES: 68
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
: ADDRESSEE: Dunner
: STREET: 1300 I Street, N.W., Suite 700
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20005-3315
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/092,077
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/472,928
: FILING DATE: 07-JUN-1995
: APPLICATION NUMBER: US 08/160,465
: FILING DATE: 02-DEC-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: FR 8912371
: FILING DATE: 20-SEP-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: FR 8907354
: FILING DATE: 06-FEB-1989
: ATTORNEY/AGENT INFORMATION:
: NAME: Meyers, Kenneth J.
: REGISTRATION NUMBER: 25,146
: REFERENCE/DOCKET NUMBER: 02356.0062-02000
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202)408-4000
: TELEFAX: (202)408-4400
: INFORMATION FOR SEQ ID NO: 45:
: SEQUENCE CHARACTERISTICS:

LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-092-077-45

Query Match 85.6%; Score 15.4; DB 3; Length 21;
Best Local Similarity 94.1%; Pred. No. 4.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGGAGGGGGAGGAGGGG 18
|||||
Db 3 TGGAGGGGGAGGAGGAG 19
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RESULT 2

US-08-529-878B-3
Sequence 3, Application US/08529878B
Patent No. 5932556

GENERAL INFORMATION:
APPLICANT: Tam, Robert C.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
REGULATION OF CD28 EXPRESSION
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:

ADDRESSEE: Crockett & Fish
STREET: 3000 S. Augusta Court
CITY: La Habra
STATE: California
COUNTRY: United States of America
ZIP: 90631

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/529,878B
FILING DATE: 13-SEP-1995
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Fish, Robert D.
REGISTRATION NUMBER: 33,880

REFERENCE/DOCKET NUMBER: 213/003

TELEPHONE: 714-525-3433

TELEFAX: 714-525-3303

TELEX:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: DNA (genomic)

US-08-529-878B-3

Query Match 82.2%; Score 14.8; DB 2; Length 18;
Best Local Similarity 88.9%; Pred. No. 8.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 TTGGAGGGGGTGTGGGG 18
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RESULT 3

US-08-529-878B-44

Sequence 44, Application US/08529878B

Patent No. 5932556

GENERAL INFORMATION:

APPLICANT: Tam, Robert C.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
REGULATION OF CD28 EXPRESSION
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:

ADDRESSEE: Crockett & Fish
STREET: 3000 S. Augusta Court
CITY: La Habra
STATE: California
COUNTRY: United States of America
ZIP: 90631

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/529,878B

FILING DATE: 13-SEP-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Fish, Robert D.

REGISTRATION NUMBER: 33,880

REFERENCE/DOCKET NUMBER: 213/003

TELEPHONE: 714-525-3433

TELEFAX: 714-525-3303

TELEX:

INFORMATION FOR SEQ ID NO: 44:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: DNA (genomic)

US-08-529-878B-44

Query Match 82.2%; Score 14.8; DB 2; Length 18;
Best Local Similarity 88.9%; Pred. No. 8.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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|||||
Db 1 TTGGAGGGGGTGTGGGG 18
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RESULT 4

US-08-529-878B-4

Sequence 4, Application US/08529878B

Patent No. 5932556

GENERAL INFORMATION:

APPLICANT: Tam, Robert C.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR

REGULATION OF CD28 EXPRESSION

NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS:

ADDRESSEE: Crockett & Fish

STREET: 3000 S. Augusta Court

CITY: La Habra

STATE: California

COUNTRY: United States of America

ZIP: 90631

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/529,878B

FILING DATE: 13-SEP-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Fish, Robert D.

REGISTRATION NUMBER: 33,880

REFERENCE/DOCKET NUMBER: 213/003
TELEPHONE: 714-525-3433
TELEFAX: 714-525-3303
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-529-878B-4

Query Match 82.2%; Score 14.8; DB 2; Length 21;
Best Local Similarity 88.9%; Pred. No. 8.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGGAGGAGGGG 18
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DB 4 TTGGAGGGGGTGGTGGGG 21
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RESULT 5

US-08-529-878B-45
Sequence 45, Application US/08529878B
Patent No. 5932556
GENERAL INFORMATION:
APPLICANT: Tam, Robert C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Crockett & Fish
STREET: 3000 S. Augusta Court
CITY: La Habra
STATE: California
COUNTRY: United States of America
ZIP: 90631

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/529,878B
FILING DATE: 13-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Fish, Robert D.
REGISTRATION NUMBER: 33,880
REFERENCE/DOCKET NUMBER: 213/003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-525-3433
TELEFAX: 714-525-3303
TELEX:

INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-529-878B-45

Query Match 82.2%; Score 14.8; DB 2; Length 21;
Best Local Similarity 88.9%; Pred. No. 8.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGGAGGAGGGG 18
|||||
DB 4 TTGGAGGGGGTGGTGGGG 21
|||||

RESULT 6
US-08-173-489C-127/c
Sequence 127, Application US/08173489C
Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
APPLICANT: HEBURN, A. G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10021.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: U9518-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (attorney) (212) 708-1880
TELEFAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 127:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
DESCRIPTION: alpha-1-globin gene (accession #
DESCRIPTION: V00491) nucleotides 827 to 843
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
AUTHORS: Michelson, A M, Orkin, S H.
TITLE: The 3' untranslated regions
TITLE: of the duplicated human alpha-globin genes are
TITLE: unexpectedly divergent
JOURNAL: Cell
VOLUME: 22
PAGES: 371-377
DATE: 1980
RELEVANT RESIDUES IN SEQ ID NO: 127 :FROM 1 TO 17
US-08-173-489C-127

Query Match 80.0%; Score 14.4; DB 2; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGGGGGAGGAGGGG 18
|||||
DB 16 GGAAGGGGGAGGAGGGG 1
|||||

RESULT 7

US-09-780-173A-93

; Sequence 93, Application US/09780173A

; Patent No. 6455307

; GENERAL INFORMATION:

; APPLICANT: Robert McKay

; APPLICANT: Susan M. Freier

; APPLICANT: Jacqueline Wyatt

; TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-ALPHA PRIME EXPRESSION

; FILE REFERENCE: RTS-0165

; CURRENT APPLICATION NUMBER: US/09/780,173A

; CURRENT FILING DATE: 2001-02-08

; NUMBER OF SEQ ID NOS: 95

; SEQ ID NO 93

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide

US-09-780-173A-93

Query Match 76.7%; Score 13.8; DB 4; Length 20;

Best Local Similarity 88.2%; Pred. No. 2e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGGAGGGGAGGAGGGG 18

Db 2 TGGAGGGGAGGAGGAG 18

RESULT 8

US-09-661-753-30/c

; Sequence 30, Application US/09661753

; Patent No. 6436909

; GENERAL INFORMATION:

; APPLICANT: Nicholas M. Dean

; APPLICANT: Susan F. Murray

; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA

; FILE REFERENCE: ISPP-0498

; CURRENT APPLICATION NUMBER: US/09/661,753

; CURRENT FILING DATE: 2000-09-14

; EARLIER APPLICATION NUMBER: 60/154,546

; EARLIER FILING DATE: 1999-09-17

; NUMBER OF SEQ ID NOS: 68

; SEQ ID NO 30

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide

US-09-661-753-30

Query Match 74.4%; Score 13.4; DB 4; Length 20;

Best Local Similarity 93.3%; Pred. No. 2.8e+03;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGAGGGGAGGAGGG 17

Db 20 GGAGGGGAGGAGGG 6

RESULT 9

US-09-495-140-26

; Sequence 26, Application US/09495140

; Patent No. 6376182

; GENERAL INFORMATION:

; APPLICANT: CHAO, LEE

; APPLICANT: CHAO, JULIE

; APPLICANT: SONG, QING

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING

; TITLE OF INVENTION: TISSUE KALLIKREIN GENE PROMOTER POLYMORPHISMS WITH TREATMENT

; TITLE OF INVENTION: OF ESSENTIAL HYPERTENSION

; FILE REFERENCE: 19113.0081

; CURRENT APPLICATION NUMBER: US/09/495,140

; CURRENT FILING DATE: 2000-01-31

; EARLIER APPLICATION NUMBER: 09/389,566

; EARLIER FILING DATE: 1999-09-03

; EARLIER APPLICATION NUMBER: 08/856,141

; EARLIER FILING DATE: 1997-05-14

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: FASTSEQ for Windows Version 4.0

; SEQ ID NO 26

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: /No. 6376182e =

; OTHER INFORMATION: synthetic construct

US-09-495-140-26

Query Match 71.1%; Score 12.8; DB 4; Length 17;

Best Local Similarity 87.5%; Pred. No. 4.7e+03;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGAGGGGAGGAGGGG 18

Db 1 GGAGGGGAGGAGGGG 16

RESULT 10

US-09-344-579-9

; Sequence 9, Application US/09344579

; Patent No. 6054316

; GENERAL INFORMATION:

; APPLICANT: Brenda F. Baker

; APPLICANT: Lex M. Cowsett

; TITLE OF INVENTION: ANTISENSE MODULATION OF ETS-2 EXPRESSION

; FILE REFERENCE: RTS-0063

; CURRENT APPLICATION NUMBER: US/09/344,579

; CURRENT FILING DATE: 1999-06-25

; NUMBER OF SEQ ID NOS: 47

; SEQ ID NO 9

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide

US-09-344-579-9

Query Match 71.1%; Score 12.8; DB 3; Length 18;

Best Local Similarity 87.5%; Pred. No. 4.7e+03;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGAGGGGAGGAGGGG 18

Db 2 GGAGGGGAGGAGGAG 17

RESULT 11

US-09-490-692-153/c

; Sequence 153, Application US/09490692

; Patent No. 6180353

; GENERAL INFORMATION:

; APPLICANT: Nicholas M. Dean

; APPLICANT: Lex M. Cowsett

; TITLE OF INVENTION: ANTISENSE MODULATION OF DAXX EXPRESSION

; FILE REFERENCE: RTS-0120

; CURRENT APPLICATION NUMBER: US/09/490,692

; CURRENT FILING DATE: 2000-01-24

; NUMBER OF SEQ ID NOS: 176

; SEQ ID NO 153

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide

US-09-490-692-153

Query Match 71.1%; Score 12.8; DB 3; Length 20;
Best Local Similarity 87.5%; Pred. No. 4.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGAGGAGGGG 18
|||||
DB 16 GGAGGAGGAGGAGG 1

RESULT 12

US-08-256-426B-282/c
; Sequence 282, Application US/08256426B
; Patent No. 5948611
; GENERAL INFORMATION:
; APPLICANT: Prockop, Darwin J.
; APPLICANT: Ala-Kokko, Leena
; APPLICANT: Williams, Charlene J.
; APPLICANT: Ritvanieni, Pertti
; APPLICANT: Baldwin, Clinton
; APPLICANT: Hopkinson, Ian
; APPLICANT: Ahmad, Nilofar Nina
; TITLE OF INVENTION: Methods of Detecting A Genetic
; CORRESPONDENCE ADDRESSES:
; NUMBER OF SEQUENCES: 293
; ADDRESS: Woodcock Washburn Kurtz Mackiewicz & No. 5948611ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 3.1
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256.426B
FILING DATE: 03-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10964
FILING DATE: 12-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,284
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Mark Deluca
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TUU-1082
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 282:
SEQUENCE CHARACTERISTICS:
LENGTH: 21
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR

Query Match 71.1%; Score 12.8; DB 2; Length 21;
Best Local Similarity 87.5%; Pred. No. 4.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGGAGGGGAGGAGG 16
|||||
DB 20 TTGGAGCAGGAGGAGG 5

RESULT 13

US-08-863-639A-41
; Sequence 41, Application US/08863639A
; Patent No. 5981185

GENERAL INFORMATION:
APPLICANT: Matson, Robert S.
APPLICANT: Coassin, Peter J.
APPLICANT: Rampal, Jang B.
APPLICANT: Caskey, C. T.
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, 9th Floor
CITY: Pasadena
STATE: CA
COUNTRY: USA
ZIP: 91101

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Corel WordPerfect 8 version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/863,639A
FILING DATE: May 28, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Joseph E. Mueth
REGISTRATION NUMBER: 20,532
REFERENCE/DOCKET NUMBER: 11859-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (626) 796-4000
TELEFAX: (626) 795-6321
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
US-08-863-639A-41

Query Match 71.1%; Score 12.8; DB 2; Length 21;
Best Local Similarity 87.5%; Pred. No. 4.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGAGGGGAGGAGGGG 18
|||||
DB 2 GGAGGAGGAGGAGGAG 17

RESULT 14

US-08-863-639A-53/c
; Sequence 53, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Corel WordPerfect 8 version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/863,639A

```

/ / FILING DATE: May 28, 1997
/ / CLASSIFICATION: 435
/ / ATTORNEY/AGENT INFORMATION:
/ / NAME: Joseph E. Mueth
/ / REGISTRATION NUMBER: 20,532
/ / REFERENCE/DOCKET NUMBER: 11859-1
/ / TELECOMMUNICATION INFORMATION:
/ / TELEPHONE: (626) 796-4000
/ / TELEFAX: (626) 795-6321
/ / INFORMATION FOR SEQ ID NO: 53:
/ / SEQUENCE CHARACTERISTICS:
/ / LENGTH: 21 base pairs
/ / TYPE: nucleic acid
/ / STRANDEDNESS: single
/ / TOPOLOGY: linear
/ / MOLCULE TYPE: Other nucleic acid
/ /
/ / US-08-863-639A-53

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Query Match 71.1%; Score 12.8; DB 2; Length 21;
Best Local Similarity 87.5%; Pred. No. 4.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels

QY 3 GCAGGGGAGGAGGG 18
DB 20 GCAGGAGGAGGAG 5

RESULT 15

US-08-863-639A-59/c
; Sequence 59, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:

APPLICANT: Matson, Robert S.
APPLICANT: Coassin, Peter J.
APPLICANT: Rampal, Jang B.
APPLICANT: Caskey, C.T.

TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS

NUMBER OF SEQUENCES: 95

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sheldon & Mak

STREET: 225 South Lake Avenue, 9th Floor

CITY: Pasadena

STATE: CA

COUNTRY: USA

ZIP: 91101

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage

COMPUTER: IBM compatible

```

/ COMPACT: 128 COMPACT: 128
; OPERATING SYSTEM: Windows 95

```

SOFTWARE: Corel WordPerfect 8 version

```

; CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/08/863,639A

FILING DATE: May 28 1997

FILED DATE: May 28
CLASSIFICATION: 435

CLASSIFICATION: 43B
ATTORNEY/AGENT INFORMATION:

NAME: Joseph E. Mueth

NAME: JOSEPH E. MUELLER
REGISTRATION NUMBER: 20,532

REGISTRATION NUMBER: 20,332
REFERENCE/DOCKET NUMBER: 11859-1

REFERENCE/ DOCUMENT NUMBER: IT
TELECOMMUNICATION INFORMATION:

TELEPHONE: (626) 796-4444

TELEPHONE: (626) 795-6332
TELEFAX: (626) 795-6332

; INFORMATION FOR SEQ ID NO: 59:

; SEQUENCE CHARACTERISTICS:

```

;
; LENGTH: 21 base pairs

```

```

;
; TYPE: nucleic acid

```

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Other nucleic acid

US-08-863-639A-59

Query Match 71.1%; Score 12.8; DB 2; Length 21;
Best Local Similarity 87.5%;
Pred. No. 4.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels

```

Qy      3 GGAGGGGAGGAGGGG 18
          | | | | | | | |
Db     19 GGAGGAGGAGGAGGAG 4

```

Search completed: October 27, 2003, 14:03:35
Job time : 42.3143 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 11:25:34 ; Search time 387.943 Seconds
(without alignments)
124.432 Million cell updates/sec

Title: US-09-331-204A-7

Perfect score: 18

Sequence: 1 ttggaggaggagagggg 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1792395 seqs, 134090451 residues

Total number of hits satisfying chosen parameters: 408622

Minimum DB seq length: 0

Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
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11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
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13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	15	83.3	17	12	US-10-061-201-1934
C 2	15	83.3	17	12	US-10-061-201-1935
C 3	15	83.3	17	12	US-10-061-201-1936
C 4	14.8	82.2	21	9	US-09-828-034-28
C 5	14	77.8	17	12	US-10-061-201-1933
C 6	14	77.8	17	12	US-10-061-201-1937
C 7	13.4	74.4	20	11	US-09-948-002-30
C 8	13	72.2	17	11	US-09-780-533A-46
C 9	13	72.2	17	11	US-09-780-533A-47
C 10	13	72.2	17	11	US-09-780-533A-899
C 11	13	72.2	17	11	US-09-780-533A-901
C 12	13	72.2	17	11	US-09-780-533A-900
C 13	13	72.2	17	12	US-10-061-201-1932
C 14	13	72.2	17	12	US-10-061-201-1938
C 15	12.8	71.1	17	11	US-09-780-533A-45
C 16	12.8	71.1	17	11	US-09-780-533A-894

C 17	12.8	71.1	17	12	US-10-059-877-26	Sequence 26, Appl
C 18	12.8	71.1	17	12	US-10-303-109A-30	Sequence 30, Appl
C 19	12.8	71.1	17	14	US-10-059-888-26	Sequence 26, Appl
C 20	12.8	71.1	20	11	US-09-918-501-11	Sequence 11, Appl
C 21	12.8	71.1	20	12	US-10-032-585-4054	Sequence 4054, App
C 22	12.8	71.1	20	14	US-10-181-846-153	Sequence 153, App
C 23	12.8	71.1	21	9	US-09-828-034-9	Sequence 9, Appl
C 24	12.4	68.9	21	14	US-10-258-860-10	Sequence 10, Appl
C 25	12.4	68.9	22	11	US-09-726-258-38	Sequence 38, Appl
C 26	12.2	67.8	17	11	US-09-780-533A-902	Sequence 902, App
C 27	12.2	67.8	17	11	US-09-930-423-866	Sequence 866, App
C 28	12.2	67.8	17	12	US-09-745-237A-866	Sequence 866, App
C 29	12.2	67.8	17	14	US-10-060-756A-685	Sequence 685, App
C 30	12.2	67.8	20	9	US-09-854-883-174	Sequence 174, App
C 31	12	66.7	17	11	US-09-780-533A-898	Sequence 898, App
C 32	12	66.7	17	12	US-10-061-201-1931	Sequence 1931, App
C 33	12	66.7	17	12	US-10-061-201-1939	Sequence 1939, App
C 34	11.8	65.6	15	14	US-10-314-405-43	Sequence 43, Appl
C 35	11.8	65.6	16	12	US-10-059-877-22	Sequence 22, Appl
C 36	11.8	65.6	16	12	US-10-339-161-26	Sequence 26, Appl
C 37	11.8	65.6	16	14	US-10-059-888-22	Sequence 22, Appl
C 38	11.8	65.6	17	11	US-09-780-533A-893	Sequence 893, App
C 39	11.8	65.6	17	11	US-09-780-533A-895	Sequence 895, App
C 40	11.8	65.6	17	11	US-09-740-332-1833	Sequence 1833, App
C 41	11.8	65.6	17	12	US-09-817-879-1833	Sequence 1833, App
C 42	11.8	65.6	18	11	US-09-940-244-161	Sequence 161, App
C 43	11.8	65.6	18	11	US-09-864-536A-218	Sequence 218, App
C 44	11.8	65.6	18	12	US-10-290-386-161	Sequence 161, App
C 45	11.8	65.6	18	12	US-10-084-839-218	Sequence 218, App

ALIGNMENTS

RESULT 1
US-10-061-201-1934/c
; Sequence 1934, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061.201
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aesomica Sequence Listing Engine
; SEQ ID NO 1934
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-1934

Query Match

83.3%; Score 15; DB 12; Length 17;

Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGGGGAGGAGGGG 18
|||
Db 17 GAGGGGGAGGAGGGG 3

RESULT 2

US-10-061-201-1935/c
; Sequence 1935, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 1935
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-1935

Query Match 83.3%; Score 15; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGGGGAGGAGGGG 18
|||
Db 16 GAGGGGGAGGAGGGG 2

RESULT 3

US-10-061-201-1936/c
; Sequence 1936, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 1936
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-1936

Query Match 83.3%; Score 15; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGGGGAGGAGGGG 18
|||
Db 15 GAGGGGGAGGAGGGG 1

RESULT 4

US-09-828-034-28/c
; Sequence 28, Application US/09828034
; Patent No. US20020064771A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Weidong
; APPLICANT: Hong, Zhi
; APPLICANT: Ferrari, Eric
; TITLE OF INVENTION: HCV REPLICASE COMPLEXES
; FILE REFERENCE: IN01165
; CURRENT APPLICATION NUMBER: US/09/828,034
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: U.S. 60/195,852
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
US-09-828-034-28

Query Match 82.2%; Score 14.8; DB 9; Length 21;
Best Local Similarity 88.9%; Pred. No. 6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGAGGAGGGG 18
|||
Db 20 TTGGAGGGGGAGGAGGAG 3

RESULT 5

US-10-061-201-1933/c
; Sequence 1933, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666

;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 09/864,761
;; PRIOR FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/328,205
;; PRIOR FILING DATE: 2001-10-10
;; NUMBER OF SEQ ID NOS: 4162
;; SOFTWARE: Aeomica Sequence Listing Engine
;; SEQ ID NO 1933
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-061-201-1933

Query Match 77.8%; Score 14; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGGGGAGGAGGGG 18
DB 17 AGGGGAGGAGGGG 4

RESULT 6
US-10-061-201-1937/c
;; Sequence 1937, Application US/10061201
;; Publication No. US2003016229A1
;; GENERAL INFORMATION:
;; APPLICANT: Shannon, Mark
;; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
;; FILE REFERENCE: P03178
;; CURRENT APPLICATION NUMBER: US/10/061,201
;; CURRENT FILING DATE: 2002-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 09/864,761
;; PRIOR FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/328,205
;; PRIOR FILING DATE: 2001-10-10
;; NUMBER OF SEQ ID NOS: 4162
;; SOFTWARE: Aeomica Sequence Listing Engine
;; SEQ ID NO 1937
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-061-201-1937

Query Match 77.8%; Score 14; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGGGAGGAGGG 17
DB 14 GAGGGGAGGAGGG 1

RESULT 7
US-09-948-002-30/c
;; Sequence 30, Application US/09948002
;; Publication No. US20030050265A1
;; GENERAL INFORMATION:
;; APPLICANT: Nicholas M. Dean
;; APPLICANT: Susan F. Murray
;; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
;; FILE REFERENCE: ISPH-0607
;; CURRENT APPLICATION NUMBER: US/09/948,002
;; CURRENT FILING DATE: 2000-09-05
;; PRIOR APPLICATION NUMBER: 09/661,753
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/154,546
;; PRIOR FILING DATE: 1999-09-17
;; NUMBER OF SEQ ID NOS: 71
;; SEQ ID NO 30
;; LENGTH: 20
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Antisense Oligonucleotide
US-09-948-002-30

Query Match 74.4%; Score 13.4; DB 11; Length 20;
Best Local Similarity 93.3%; Pred. No. 2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGGGAGGAGGG 17
DB 20 GGAGGGGAGGAGGG 6

RESULT 8
US-09-780-533A-46/c
;; Sequence 46, Application US/09780533A
;; Publication No. US20030060611A1
;; GENERAL INFORMATION:
;; APPLICANT: Ribozyne Pharmaceuticals, Inc.
;; APPLICANT: Blatt, Larry
;; APPLICANT: McSwiggen, Jim
;; APPLICANT: Chowrika, Bharat
;; APPLICANT: Haerberli, Pete
;; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
;; FILE REFERENCE: MBH00,878-A (400/011)
;; CURRENT APPLICATION NUMBER: US/09/780,533A
;; CURRENT FILING DATE: 2001-02-09
;; PRIOR APPLICATION NUMBER: US 60/181,797
;; PRIOR FILING DATE: 2000-02-11
;; NUMBER OF SEQ ID NOS: 6679
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 46
;; LENGTH: 17
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-09-780-533A-46

Query Match 72.2%; Score 13; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGGGAGGAGGGG 18

```
Db      16 GGGGGAGGAGGGG 4
|||||
RESULT 9
US-09-780-533A-47/c
; Sequence 47, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00.878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-47

Query Match      72.2%; Score 13; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GGGGGAGGAGGGG 18
Db      13 GGGGGAGGAGGGG 1
|||||
RESULT 10
US-09-780-533A-899/c
; Sequence 899, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00.878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 899
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-899

Query Match      72.2%; Score 13; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GGGGGAGGAGGGG 18
Db      17 GGGGGAGGAGGGG 5
|||||
RESULT 11
US-09-780-533A-900/c
; Sequence 900, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00.878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 900
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-900

Query Match      72.2%; Score 13; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GGGGGAGGAGGGG 18
Db      15 GGGGGAGGAGGGG 3
|||||
RESULT 12
US-09-780-533A-901/c
; Sequence 901, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00.878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 901
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-901

Query Match      72.2%; Score 13; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GGGGGAGGAGGGG 18
Db      14 GGGGGAGGAGGGG 2
|||||
RESULT 13
US-10-061-201-1932/c
; Sequence 1932, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PEO178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Ascomica Sequence Listing Engine
; SEQ ID NO 1932
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-1932

Query Match      72.2%; Score 13; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GGGGGAGGAGGGG 18
      |||||
DB      17 GGGGGAGGAGGGG 5

RESULT 14
US-10-061-201-1938/c
; Sequence 1938, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061.201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Ascomica Sequence Listing Engine
; SEQ ID NO 1938
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens

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US-10-061-201-1938

Query Match      72.2%; Score 13; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 GAGGGGAGGAGG 16
      |||||
DB      13 GAGGGGAGGAGG 1

RESULT 15
US-09-780-533A-45/c
; Sequence 45, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: MCSwigen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MEH800.878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-45

Query Match      71.1%; Score 12.8; DB 11; Length 17;
Best Local Similarity 87.5%; Pred. No. 3.6e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 GGAGGGGAGGAGGGG 18
      |||||
DB      16 GGAGGGGAGGCGGG 1

Search completed: October 27, 2003, 19:00:53
Job time : 387.943 secs

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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:35 ; Search time 2356.29 Seconds
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Title: US-09-331-204A-7
Perfect score: 18
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 33363688 seqs, 1658189874 residues
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database : Pending Parents NA Main:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	18	100.0	18	US-09-331-204A-7
2	18	100.0	19	US-09-331-204-4
3	17	94.4	19	US-10-310-188-47425
4	16.4	91.1	18	US-09-331-204-5


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; PRIOR APPLICATION NUMBER: PCT/US97/23927
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: An oligomer
; OTHER INFORMATION: or polymer of ribonucleic acid or deoxyribonucleic
; OTHER INFORMATION: acid. This term includes oligomers consisting of
; OTHER INFORMATION: naturally occurring bases, sugars and intersugar (
US-09-331-204-5

Query Match          91.1%; Score 16.4; DB 19; Length 18;
Best Local Similarity 94.4%; Pred. No. 2.7e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGAGGAGGGG 18
Db 1 TTGGAGGGGGAGGTGGG 18

RESULT 5
US-09-331-204A-8
; Sequence 8, Application US/09331204A
; GENERAL INFORMATION:
; APPLICANT: ICN Pharmaceuticals, Inc.
; APPLICANT: Tam, Robert
; TITLE OF INVENTION: G-rich Oligo Aptamers and Methods of Modulating an Immune Respo
; FILE REFERENCE: 216/013-US1
; CURRENT APPLICATION NUMBER: US/09/331,204A
; CURRENT FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US97/23927
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 8
; LENGTH: 18
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-331-204A-8

Query Match          91.1%; Score 16.4; DB 19; Length 18;
Best Local Similarity 94.4%; Pred. No. 2.7e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGAGGAGGGG 18
Db 1 TTGGAGGGGGAGGTGGG 18

RESULT 6
US-08-472-928B-45
; Sequence 45, Application US/08472928B
; GENERAL INFORMATION:
; APPLICANT: Montagnier, Luc
; APPLICANT: Montagnier, Luc
; TITLE OF INVENTION: Nucleotide Sequences Derived From The
; TITLE OF INVENTION: Genome Of Retroviruses Of The HIV-1, HIV-2 And SIV Type,
; TITLE OF INVENTION: And Their Uses In Particular For The Amplification Of The
; TITLE OF INVENTION: Genomes Of These Retroviruses And For The In Vitro Diagnosis
; TITLE OF INVENTION: Of The Diseases Due To Those Viruses
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESS: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,928B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160,465
; FILING DATE: 02-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 8912371
; FILING DATE: 20-SEP-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 8907354
; FILING DATE: 06-FEB-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0062-02000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)408-4000
; TELEFAX: (202)408-4400
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-472-928B-45

Query Match          85.6%; Score 15.4; DB 9; Length 21;
Best Local Similarity 94.1%; Pred. No. 6.4e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGGAGGGGGAGGAGGGG 18
Db 3 TGGAGGGGGAGGAGGAG 19

RESULT 7
US-09-670-105-45
; Sequence 45, Application US/09670105
; GENERAL INFORMATION:
; APPLICANT: Montagnier, Luc
; APPLICANT: Montagnier, Luc
; TITLE OF INVENTION: Nucleotide Sequences Derived From The
; TITLE OF INVENTION: Genome Of Retroviruses Of The HIV-1, HIV-2 And SIV Type,
; TITLE OF INVENTION: And Their Uses In Particular For The Amplification Of The
; TITLE OF INVENTION: Genomes Of These Retroviruses And For The In Vitro Diagnosis
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESS: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/670,105
; FILING DATE: 26-Sep-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/092,077

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FILING DATE: <Unknown>
APPLICATION NUMBER: US/08/472,928
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US/08/160,465
FILING DATE: 02-DEC-1993
APPLICATION NUMBER: FR 8912371
FILING DATE: 20-SEP-1989
APPLICATION NUMBER: FR 8907354
FILING DATE: 06-FEB-1989
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0062-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)408-4000
TELEFAX: (202)408-4400
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-670-103-45

Query Match 85.6%; Score 15.4; DB 29; Length 21;
Best Local Similarity 94.1%; Pred. No. 6.4e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGGAGGGGAGGAGGGG 18
DB 3 TGGAGGGGAGGAGGAG 19

RESULT 8
US-10-061-201-1934/c
; Sequence 1934, Application US/10061201
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1934
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-1934

Query Match 83.3%; Score 15; DB 45; Length 17;

Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GAGGGGAGGAGGGG 18
DB 17 GAGGGGAGGAGGGG 3

RESULT 9
US-10-061-201-1935/c
; Sequence 1935, Application US/10061201
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1935
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-1935

Query Match 83.3%; Score 15; DB 45; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGGGAGGAGGGG 18
DB 16 GAGGGGAGGAGGGG 2

RESULT 10
US-10-061-201-1936/c
; Sequence 1936, Application US/10061201
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30

;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 09/864,761
;; PRIOR FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/328,205
;; PRIOR FILING DATE: 2001-10-10
;; NUMBER OF SEQ ID NOS: 4162
;; SOFTWARE: Aecomica Sequence Listing Engine
;; SEQ ID NO 1936
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-061-201-1936

Query Match 83.3%; Score 15; DB 45; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGGGAGGAGGGG 18
Db 15 GAGGGGAGGAGGGG 1

RESULT 11
US-60-328-205-1934/c
;; Sequence 1934, Application US/60328205
;; GENERAL INFORMATION:
;; APPLICANT: Shannon, Mark
;; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
;; FILE REFERENCE: AECOMICA-26
;; CURRENT APPLICATION NUMBER: US/60/328,205
;; CURRENT FILING DATE: 2001-10-10
;; NUMBER OF SEQ ID NOS: 4162
;; SOFTWARE: Aecomica Sequence Listing Engine
;; SEQ ID NO 1934
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-60-328-205-1934

Query Match 83.3%; Score 15; DB 87; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGGGAGGAGGGG 18
Db 17 GAGGGGAGGAGGGG 3

RESULT 12
US-60-328-205-1935/c
;; Sequence 1935, Application US/60328205
;; GENERAL INFORMATION:
;; APPLICANT: Shannon, Mark
;; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
;; FILE REFERENCE: AECOMICA-26
;; CURRENT APPLICATION NUMBER: US/60/328,205
;; CURRENT FILING DATE: 2001-10-10
;; NUMBER OF SEQ ID NOS: 4162
;; SOFTWARE: Aecomica Sequence Listing Engine
;; SEQ ID NO 1935
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-60-328-205-1935

Query Match 83.3%; Score 15; DB 87; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGGGAGGAGGGG 18
Db 16 GAGGGGAGGAGGGG 2

RESULT 13
US-60-328-205-1936/c
;; Sequence 1936, Application US/60328205
;; GENERAL INFORMATION:
;; APPLICANT: Shannon, Mark
;; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
;; FILE REFERENCE: AECOMICA-26
;; CURRENT APPLICATION NUMBER: US/60/328,205
;; CURRENT FILING DATE: 2001-10-10
;; NUMBER OF SEQ ID NOS: 4162
;; SOFTWARE: Aecomica Sequence Listing Engine
;; SEQ ID NO 1936
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-60-328-205-1936

Query Match 83.3%; Score 15; DB 87; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGGGGAGGAGGGG 18
Db 15 GAGGGGAGGAGGGG 1

RESULT 14
US-10-310-188-6227/c
;; Sequence 6227, Application US/10310188
;; GENERAL INFORMATION:
;; APPLICANT: RosettaGenomics
;; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN
;; FILE REFERENCE: 47487
;; CURRENT APPLICATION NUMBER: US/10/310,188
;; CURRENT FILING DATE: 2002-12-19
;; NUMBER OF SEQ ID NOS: 86841
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 6227
;; LENGTH: 18
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-310-188-6227

Query Match 83.3%; Score 15; DB 50; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGAGGGGAGGAGGGG 17
Db 15 GGAGGGGAGGAGGGG 1

RESULT 15
US-10-303-778-16894
;; Sequence 16894, Application US/10303778
;; GENERAL INFORMATION:
;; APPLICANT: RosettaGenomics
;; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL
;; FILE REFERENCE: 47416
;; CURRENT APPLICATION NUMBER: US/10/303,778
;; CURRENT FILING DATE: 2002-11-26
;; NUMBER OF SEQ ID NOS: 17608
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 16894
;; LENGTH: 19

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-778-16894

Query Match      83.3%   Score 15; DB 50; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GGAGGGGGGAGGAGG 17
         |||||
Db       4 GGAGGGGGGAGGAGG 18

Search completed: October 27, 2003, 17:52:53
Job time : 2356.29 secs
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GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:29 ; Search time 162 Seconds
(without alignments)
299.938 Million cell updates/sec

Title: US-09-331-204A-7

Perfect score: 18

Sequence: 1 ttggaagggagagagggg 18

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 1643990

Minimum DB seq length: 0

Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 25: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	17	CD28 expression in
2	18	100.0	18	20	CD28 inhibiting ph
3	16.4	91.1	18	17	CD28 expression in
4	16.4	91.1	18	20	CD28 inhibiting ph
5	15.4	85.6	21	11	MMY24 nucleotide c
6	15.4	85.6	21	18	Human or simian im
7	15	83.3	17	24	Human POSHL1 scann
8	15	83.3	17	24	Human POSHL1 scann

C	9	15	83.3	17	24	ABV91223	Human POSHL1 scann
	10	14.8	82.2	18	17	AAT36196	Triplex forming ol
	11	14.8	82.2	18	20	AAK90328	CD28 inhibiting ph
	12	14.8	82.2	18	20	AAK90290	CD28 inhibiting ol
	13	14.8	82.2	18	21	AAZ99625	Nucleotide sequenc
	14	14.8	82.2	18	21	AAZ99650	Nucleotide sequenc
C	15	14.8	82.2	21	17	AAT36197	Triplex forming ol
	16	14.8	82.2	21	20	AAK90329	CD28 inhibiting ph
	17	14.8	82.2	21	20	AAK90291	CD28 inhibiting ol
	18	14.8	82.2	21	24	ABK99294	Hepatitis C virus
	19	14.4	80.0	17	20	AAK14740	Triple helix formi
C	20	14	77.8	17	24	ABV91220	Human POSHL1 scann
	21	14	77.8	17	24	ABV91224	Human POSHL1 scann
C	22	13.8	76.7	20	24	ABK00899	Human POSHL1 scann
	23	13.6	75.6	22	22	AAK67915	Gastric acid produ
	24	13.4	74.4	21	20	AAK32871	TFO B13 sequence.
	25	13.2	73.3	20	22	AAH50875	Human tumour assoc
C	26	13.2	73.3	20	22	ADK03330	RNL primer used to
	27	13	72.2	17	23	ABK00046	Human NOGO Hammerh
C	28	13	72.2	17	23	ABK00047	Human NOGO Hammerh
	29	13	72.2	17	23	ABK00899	Human NOGO inozyme
C	30	13	72.2	17	23	ABK00900	Human NOGO inozyme
	31	13	72.2	17	23	ABK00901	Human NOGO inozyme
C	32	13	72.2	17	24	ABV91219	Human POSHL1 scann
	33	13	72.2	17	24	ABV91225	Human POSHL1 scann
C	34	12.8	71.1	17	20	ABV55680	Human tissue kall
	35	12.8	71.1	17	21	AAF01954	Hammerhead ribozym
C	36	12.8	71.1	17	21	AAF05272	Hammerhead ribozym
	37	12.8	71.1	17	21	AAA25277	Oestrogen receptor
C	38	12.8	71.1	17	23	ABK00045	Human NOGO Hammerh
	39	12.8	71.1	17	23	ABK00894	Human NOGO inozyme
C	40	12.8	71.1	17	24	AAK43484	Human tissue kall
	41	12.8	71.1	18	21	AAK39350	Human Ets-2 phosph
	42	12.8	71.1	20	15	AAQ55605	3' flanking sequen
C	43	12.8	71.1	20	21	AAK60760	Human psoriasis-li
	44	12.8	71.1	20	21	AAK62403	Human psoriasis-li
C	45	12.8	71.1	20	21	AAA88033	Feline immunodefec

ALIGNMENTS

RESULT 1	AAK36242	
ID	AAK36242 standard; DNA; 18 BP.	
XX	AAK36242;	
AC	AAK36242;	
XX	25-MAR-2003 (updated)	
DT	16-APR-1997 (first entry)	
XX	CD28 expression inhibiting oligonucleotide, RT05s.	
DE	Reduction; T cell; CD28; gene expression; treatment; immune system;	
XX	disorder; graft versus host disease; septic shock; viral disease;	
XX	psoriasis; type I diabetes mellitus; thyroiditis; sarcoidosis;	
XX	multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2;	
XX	systemic lupus erythematosus; inflammatory bowel disease;	
XX	IL-2; production; antisense; inhibition; ss	
OS	Synthetic.	
XX	WO9624380-A1.	
PN	15-AUG-1996.	
XX	96WO-US01507.	
PD	05-FEB-1996;	
XX	95US-0387041.	
PF	95US-0529878.	
XX	95US-0387041.	
PR	09-FEB-1995;	
XX	95US-0529878.	
PR	09-FEB-1995;	
XX	95US-0529878.	

```

PA (ICNC ) ICN PHARM INC.
XX
XX Tam RC;
XX
XX WPI; 1996-384228/38.
XX
XX Oligo:nucleotide which reduces CD28 gene expression in T cells -
PT for treating immune system diseases, e.g. graft vs. host disease,
PT septic shock, psoriasis, etc.
XX
XX Example 2; Page 45; 77pp; English.
XX
XX The present oligonucleotide reduces CD28 dependent interleukin-2
CC (IL-2) production and T cell CD28 gene expression, useful in the
CC treatment of CD28 mediated diseases, particularly immune system
CC disorders, e.g. graft versus host disease, septic shock, viral
CC disease, psoriasis, type I diabetes mellitus, thyroiditis,
CC sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis,
CC systemic lupus erythematosus, inflammatory bowel disease, etc..
CC Reducing CD28 expression may reduce the effects of antigenic
CC stimulation of CD28 positive T cells, with a consequent reduction
CC in cytokine release.
CC (Updated on 25-MAR-2003 to correct PR field.)
XX
XX Sequence 18 BP; 3 A; 0 C; 13 G; 2 T; 0 other;
XX
XX Query Match 100.0%; Score 18; DB 17; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 5e+02;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 TTGGAGGGGGAGGAGGGG 18
Db 1 TTGGAGGGGGAGGAGGGG 18
XX
XX RESULT 2
XX AAX90335
XX ID AAX90335 standard; DNA; 18 BP.
XX
XX AC AAX90335;
XX
XX DT 24-SEP-1999 (first entry)
XX
XX DE CD28 inhibiting phosphorothioate oligonucleotide RT05S.
XX
XX DE CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
XX immune system mediated disease; gamma-interferon; IL-8;
XX phosphorothioate; ss.
XX
XX OS Synthetic.
XX
XX PN US5932556-A.
XX
XX PD 03-AUG-1999.
XX
XX PF 18-SEP-1995; 95US-0529878.
XX
XX PR 18-SEP-1995; 95US-0529878.
XX
XX PA (TAMR/) TAM R C.
XX
XX PI Tam RC;
XX
XX WPI; 1999-443609/37.
XX
XX Treatment of immune system-mediated diseases by inhibiting
PT expression of CD28, IL-2, gamma-interferon or IL-8
XX
XX Example; Column 24; 45pp; English.
XX
XX The present invention describes a method for inhibiting the expression
CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
CC comprises subcutaneous administration of an oligonucleotide (OGN).
CC

```

```

CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
CC method. The OGNs are used for the treatment of immune system-mediated
CC diseases. The present sequence represents a CD28 inhibiting
CC phosphorothioate oligonucleotide used in the exemplification of the
CC present invention.
XX
XX Sequence 18 BP; 3 A; 0 C; 13 G; 2 T; 0 other;
XX
XX Query Match 100.0%; Score 18; DB 20; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 5e+02;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 TTGGAGGGGGAGGAGGGG 18
Db 1 TTGGAGGGGGAGGAGGGG 18
XX
XX RESULT 3
XX AAT36243
XX ID AAT36243 standard; DNA; 18 BP.
XX
XX AC AAT36243;
XX
XX DT 25-MAR-2003 (updated)
XX
XX DT 16-APR-1997 (first entry)
XX
XX DE CD28 expression inhibiting oligonucleotide, RT09S.
XX
XX Reduction; T cell; CD28; gene expression; treatment; immune system;
XX disorder; graft versus host disease; septic shock; viral disease;
XX psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;
XX multiple sclerosis; uveitis; rheumatoid arthritis; interleukin 2;
XX systemic lupus erythematosus; inflammatory bowel disease;
XX IL-2; production; antisense; inhibition; ss
XX
XX OS Synthetic.
XX
XX PN WO9624380-A1.
XX
XX PD 15-AUG-1996.
XX
XX PF 05-FEB-1996; 96WO-US01507.
XX
XX PR 09-FEB-1995; 95US-0387041.
XX
XX PR 18-SEP-1995; 95US-0529878.
XX
XX PR 09-FEB-1995; 95US-0387041.
XX
XX PR 18-SEP-1995; 95US-0529878.
XX
XX PA (ICNC ) ICN PHARM INC.
XX
XX PI Tam RC;
XX
XX WPI; 1996-384228/38.
XX
XX Oligo:nucleotide which reduces CD28 gene expression in T cells -
PT for treating immune system diseases, e.g. graft vs. host disease,
PT septic shock, psoriasis, etc.
XX
XX Example 2; Page 45; 77pp; English.
XX
XX The present oligonucleotide reduces CD28 dependent interleukin-2
CC (IL-2) production and T cell CD28 gene expression, useful in the
CC treatment of CD28 mediated diseases, particularly immune system
CC disorders, e.g. graft versus host disease, septic shock, viral
CC disease, psoriasis, type I diabetes mellitus, thyroiditis,
CC sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis,
CC systemic lupus erythematosus, inflammatory bowel disease, etc..
CC Reducing CD28 expression may reduce the effects of antigenic
CC stimulation of CD28 positive T cells, with a consequent reduction
CC in cytokine release.
CC (Updated on 25-MAR-2003 to correct PR field.)
XX
XX Sequence 18 BP; 2 A; 0 C; 13 G; 3 T; 0 other;
XX

```

Query Match 91.1%; Score 16.4; DB 17; Length 18;
 Best Local Similarity 94.4%; Pred. No. 2e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGAGGGGAGGAGGGG 18
 DB 1 TTGGAGGGGAGGTTGGG 18

RESULT 4
 AAX90336
 ID AAX90336 standard; DNA; 18 BP.
 AC AAX90336;
 XX
 XX 24-SEP-1999 (first entry)
 DT
 XX CD28 inhibiting phosphorothioate oligonucleotide RT09S.
 DE
 XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
 KW immune system mediated disease; gamma-interferon; IL-8;
 XX phosphorothioate; ss.
 XX Synthetic.
 OS
 XX US932556-A.
 PN
 XX 03-AUG-1999.
 PD
 XX 18-SEP-1995; 95US-0529878.
 PF
 XX 18-SEP-1995; 95US-0529878.
 PR
 XX (TAMR) TAM R C.
 PA
 XX Tam RC;
 PI
 XX WPI; 1999-443609/37.
 DR
 XX Treatment of immune system-mediated diseases by inhibiting
 PT expression of CD28, IL-2, gamma-interferon or IL-8
 XX
 XX Example; Column 24; 45pp; English.

The present invention describes a method for inhibiting the expression
 of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
 comprises subcutaneous administration of an oligonucleotide (OGN).
 CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
 CC method. The OGNs are used for the treatment of immune system-mediated
 CC diseases. The present sequence represents a CD28 inhibiting
 CC phosphorothioate oligonucleotide used in the exemplification of the
 CC present invention.
 XX
 XX Sequence 18 BP; 2 A; 0 C; 13 G; 3 T; 0 other;

Query Match 91.1%; Score 16.4; DB 20; Length 18;
 Best Local Similarity 94.4%; Pred. No. 2e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGGAGGGGAGGAGGGG 18
 DB 1 TTGGAGGGGAGGTTGGG 18

RESULT 5
 AAQ06932
 ID AAQ06932 standard; DNA; 21 BP.
 XX
 AC AAQ06932;
 XX
 XX 09-JAN-2003 (updated)
 DT 05-MAR-1991 (first entry)

XX MM24 nucleotide constituent of vpx gene of HIV-2 ROD
 DE and SIV-MAC.
 XX HIV-2; SIV; AIDS; anti-sense nucleotide; ss.
 XX Human immunodeficiency virus.
 OS Simian immunodeficiency virus.
 XX EP40333-A.
 PN
 XX 19-DEC-1990.
 PD
 XX 05-JUN-1990; 90EP-0401520.
 PF
 XX 20-SEP-1989; 89FR-0012371.
 PR
 XX (INSP) INST PASTEUR.
 PA (INRM) INSERM INST NAT SANTE RE.
 XX Moncany M, Montagnier L;
 PI WPI; 1990-378039/51.
 DR
 XX New nucleotide sequences derived from genome of HIV-1, HIV-2 and
 PT SIV - useful as primers for amplification of immuno-deficiency
 PT viruses in diagnosis and for raising antibodies in treatment of
 PT HIV infections
 XX
 XX Claim 7; page 20; 24pp; French.

XX This nucleotide sequence is found in posn. 6228-6208 of HIV-2 ROD
 CC and 6141-6121 of SIV-MAC. It is the anti-sense strand of a primer
 CC pair used to amplify these HIV-1, HIV-2 and SIV viral sequences.
 CC esp in conjunction with in vitro diagnosis of infection. It is
 CC useful for treating viral diseases, eg. AIDS.
 CC See also AAQ06905-31 and AAQ06933-54.
 CC (Updated on 09-JAN-2003 to add missing OS field.)
 XX
 XX Sequence 21 BP; 5 A; 2 C; 13 G; 1 T; 0 other;

Query Match 85.6%; Score 15.4; DB 11; Length 21;
 Best Local Similarity 94.1%; Pred. No. 4.5e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGGAGGGGAGGAGGGG 18
 DB 3 TGGAGGGGAGGAGGAG 19

RESULT 6
 AAT98040
 ID AAT98040 standard; DNA; 21 BP.
 XX
 AC AAT98040;
 XX
 XX 25-MAR-2003 (updated)
 DT 08-SEP-1998 (first entry)
 XX
 XX Human or simian immunodeficiency virus detection primer MM24.
 DE
 XX Primer; PCR; amplification; gag; vpr; pol; vpu; HIV-1; HIV-2; SIV; nef2;
 KW vif2; vpx; detection; ss.
 XX
 XX Synthetic.
 OS Human immunodeficiency virus.
 OS Simian immunodeficiency virus.
 XX EP806484-A2.
 PN
 XX 12-NOV-1997.
 PD
 XX 05-JUN-1990; 97EP-0110543.
 PF

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XX 02-JUN-1989; 89PR-0007354.
PR 20-SEP-1989; 89PR-0012371.
PR 05-JUN-1990; 90EP-0401520.
XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA (INSP ) INST PASTEUR.
XX Moncany M, Montagnier L;
PI WPI; 1997-538622/50.
DR
XX Oligo-nucleotide primers for amplifying retroviral nucleic acids -
PT comprising conserved sequences of human immunodeficiency virus and
PT simian immunodeficiency virus genes
XX Claim 10; Page 21; 23pp; French.
XX The oligonucleotides AAT98010-T98059 are useful as primers for nucleic
CC acid amplification of conserved sequences of the gag, vpr, pol or vpu
CC genes of the HIV-1 strains Bru, Mal, Eli, HIV-2 ROD or simian
CC immunodeficiency virus (SIV) MAC or the nef2, vif2 or vpx genes of HIV-2
CC ROD and SIV MAC. This primer is targetted to sequences in the vpx gene of
CC the viral strains. The sequences are therefore used to detect HIV-1,
CC HIV-2 or SIV infections
CC (Updated on 25-MAR-2003 to correct PF field.)
CC (Updated on 25-MAR-2003 to correct PR field.)
XX Sequence 21 BP; 5 A; 2 C; 13 G; 1 T; 0 other;
SQ
Query Match 85.6%; Score 15.4; DB 18; Length 21;
Best Local Similarity 94.1%; Pred. No. 4.5e-03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 TCGAGGGGAGGAGGGG 18
DB 3 TCGAGGGGAGGAGGAGG 19
RESULT 7
ABV91221/c
ID ABV91221 standard; DNA; 17 BP.
XX AC ABV91221;
XX 23-DEC-2002 (first entry)
XX Human POSHL1 scanning oligonucleotide SEQ ID NO 1934.
XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
XX Rho GTPase; signal transduction; gene expression; cancer; vaccine;
XX gene therapy; transgenic; ss.
XX Homo sapiens.
XX EP1239051-A2.
XX 11-SEP-2002.
XX 28-JAN-2002; 2002EP-0001165.
XX 30-JAN-2001; 2001WO-US00663.
XX 30-JAN-2001; 2001WO-US00664.
XX 30-JAN-2001; 2001WO-US00665.
XX 30-JAN-2001; 2001WO-US00666.
XX 30-JAN-2001; 2001WO-US00667.
XX 30-JAN-2001; 2001WO-US00668.
XX 30-JAN-2001; 2001WO-US00669.
XX 30-JAN-2001; 2001WO-US00670.
XX 23-MAY-2001; 2001US-0864761.
XX 10-OCT-2001; 2001US-0328205.
XX (AEOW-) AEOMICA INC.
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XX Shannon M;
PI WPI; 2002-684061/74.
DR
XX Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide,
PT POSHL-1, useful for treating disorders associated with decreased
PT expression or activity of human POSHL1 -
XX Example 2; SEQ ID NO 1934; 60pp + Sequence Listing; English.
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC acids (SI, ABB93999), a sequence having 65% sequence identity to (SI),
CC (SI) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (II) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention.
CC Note: The present sequence did not form part of the printed
CC specification, but is based on sequence information supplied to Derwent
CC by the European Patent Office.
XX Sequence 17 BP; 1 A; 12 C; 0 G; 4 T; 0 other;
SQ
Query Match 83.3%; Score 15; DB 24; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.5e-03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GAGGGGGAGGAGGGG 18
DB 17 GAGGGGGAGGAGGGG 3
RESULT 8
ABV91222/c
ID ABV91222 standard; DNA; 17 BP.
XX AC ABV91222;
XX 23-DEC-2002 (first entry)
XX Human POSHL1 scanning oligonucleotide SEQ ID NO 1935.
XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
XX Rho GTPase; signal transduction; gene expression; cancer; vaccine;
XX gene therapy; transgenic; ss.
XX Homo sapiens.
XX EP1239051-A2.
XX 11-SEP-2002.
XX 28-JAN-2002; 2002EP-0001165.
XX 30-JAN-2001; 2001WO-US00663.
XX 30-JAN-2001; 2001WO-US00664.
XX 30-JAN-2001; 2001WO-US00665.
XX 30-JAN-2001; 2001WO-US00666.
XX 30-JAN-2001; 2001WO-US00667.
XX 30-JAN-2001; 2001WO-US00668.
XX 30-JAN-2001; 2001WO-US00669.
XX 30-JAN-2001; 2001WO-US00670.
XX 23-MAY-2001; 2001US-0864761.
XX 10-OCT-2001; 2001US-0328205.
XX (AEOW-) AEOMICA INC.
```

PR 23-MAY-2001; 2001US-0864761.
 PR 10-OCT-2001; 2001US-0328205.
 XX (AEOM-) AEOMICA INC.
 PA Shannon M;
 XX WPI; 2002-684061/74.
 DR
 XX
 XX Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide,
 PT POSHL-1, useful for treating disorders associated with decreased
 PT expression or activity of human POSHL1
 XX
 XX Example 2; SEQ ID NO 1935; 60pp + Sequence Listing; English.
 PS
 XX The invention relates to an isolated SH3 domain (POSH)-like signalling
 CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
 CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
 CC (S1) having 95% deviations, especially conservative substitutions or a
 CC fragment of the sequences comprising at least 8 contiguous amino acids.
 CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
 CC adaptor protein that interacts with Rho family small GTPases as well as
 CC downstream components of the signal transduction pathway. (I) is useful
 CC for identifying a specific binding partner. (I) and nucleic acids (II)
 CC encoding (I) are useful for diagnosing, monitoring disease and treating
 CC caused by altered expression of human POSHL1 including diagnosing and
 CC treating cancer, they useful in the development of vaccines and (II) is
 CC useful in gene therapy. (II) is useful for constructing microarrays which
 CC are useful for measuring and for surveying gene expression and creating
 CC transgenic non-human animals capable of producing the proteins. The
 CC present sequence is that of a scanning oligonucleotide useful in examples
 CC of the invention.
 CC Note: The present sequence did not form part of the printed
 CC specification, but is based on sequence information supplied to Derwent
 CC by the European Patent Office.
 XX
 SQ Sequence 17 BP; 1 A; 12 C; 0 G; 4 T; 0 other;
 Query Match 83.3%; Score 15; DB 24; Length 17;
 Best Local Similarity 100.0%; Pred. No. 6.5e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 GAGGGGGAGGAGGGG 18
 DB 16 GAGGGGGAGGAGGGG 2
 RESULT 9
 ABV91223/C
 ID ABV91223 standard; DNA; 17 BP.
 AC ABV91223;
 XX
 XX 23-DEC-2002 (first entry)
 DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1936.
 XX
 XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
 KW Rho GTPase; signal transduction; Gene expression; cancer; vaccine;
 KW gene therapy; transgenic; ss.
 XX
 XX Homo sapiens.
 XX
 XX EP1239051-A2.
 PN
 PD 11-SEP-2002.
 XX
 PF 28-JAN-2002; 2002EP-0001165.
 XX
 PR 30-JAN-2001; 2001WO-US00663.
 PR 30-JAN-2001; 2001WO-US00664.
 PR 30-JAN-2001; 2001WO-US00665.
 PR 30-JAN-2001; 2001WO-US00666.

PR 30-JAN-2001; 2001WO-US00667.
 PR 30-JAN-2001; 2001WO-US00668.
 PR 30-JAN-2001; 2001WO-US00669.
 PR 30-JAN-2001; 2001WO-US00670.
 PR 23-MAY-2001; 2001US-0864761.
 PR 10-OCT-2001; 2001US-0328205.
 XX (AEOM-) AEOMICA INC.
 XX Shannon M;
 XX WPI; 2002-684061/74.
 DR
 XX
 XX Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide,
 PT POSHL-1, useful for treating disorders associated with decreased
 PT expression or activity of human POSHL1
 XX
 XX Example 2; SEQ ID NO 1936; 60pp + Sequence Listing; English.
 PS
 XX The invention relates to an isolated SH3 domain (POSH)-like signalling
 CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
 CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
 CC (S1) having 95% deviations, especially conservative substitutions or a
 CC fragment of the sequences comprising at least 8 contiguous amino acids.
 CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
 CC adaptor protein that interacts with Rho family small GTPases as well as
 CC downstream components of the signal transduction pathway. (I) is useful
 CC for identifying a specific binding partner. (I) and nucleic acids (II)
 CC encoding (I) are useful for diagnosing, monitoring disease and treating
 CC caused by altered expression of human POSHL1 including diagnosing and
 CC treating cancer, they useful in the development of vaccines and (II) is
 CC useful in gene therapy. (II) is useful for constructing microarrays which
 CC are useful for measuring and for surveying gene expression and creating
 CC transgenic non-human animals capable of producing the proteins. The
 CC present sequence is that of a scanning oligonucleotide useful in examples
 CC of the invention.
 CC Note: The present sequence did not form part of the printed
 CC specification, but is based on sequence information supplied to Derwent
 CC by the European Patent Office.
 XX
 SQ Sequence 17 BP; 1 A; 12 C; 1 G; 3 T; 0 other;
 Query Match 83.3%; Score 15; DB 24; Length 17;
 Best Local Similarity 100.0%; Pred. No. 6.5e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 GAGGGGGAGGAGGGG 18
 DB 15 GAGGGGGAGGAGGGG 1
 RESULT 10
 AAT36196
 ID AAT36196 standard; DNA; 18 BP.
 AC AAT36196;
 XX
 XX 25-MAR-2003 (updated)
 DT 15-APR-1997 (first entry)
 DE
 XX Triplex forming oligo targeting CD28 5'-UTR (nt 58-75).
 XX
 XX Reduction; T cell; CD28; Gene expression; treatment; immune system;
 KW disorder; graft versus host disease; septic shock; viral disease;
 KW psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;
 KW multiple sclerosis; uveitis; rheumatoid arthritis; 5'-UTR;
 KW systemic lupus erythematosus; inflammatory bowel disease; ss
 KW triplex forming; oligonucleotide; 5'-untranslated region; ss
 XX
 OS Synthetic.
 XX
 XX WO9624380-A1.
 PN
 XX

PD 15-AUG-1996.
 XX 05-FEB-1996; 96WO-US01507.
 XX 09-FEB-1995; 95US-0387041.
 XX 18-SEP-1995; 95US-0529878.
 XX 09-FEB-1995; 95US-0387041.
 XX 18-SEP-1995; 95US-0529878.
 XX (ICNC) ICN PHARM INC.
 XX Tam RC;
 XX WPI; 1996-384228/38.
 XX Oligo-nucleotide which reduces CD28 gene expression in T cells -
 PT for treating immune system diseases, e.g. graft vs. host disease,
 PT septic shock, psoriasis, etc.
 XX Claim 9; Page 54; 77pp; English.
 XX The present invention describes a method for inhibiting the expression,
 CC useful in the treatment of CD28 mediated diseases, particularly
 CC immune system disorders, e.g. graft versus host disease, septic
 CC shock, viral disease, psoriasis, type I diabetes mellitus, rheumatoid
 CC arthritis, sarcoidosis, multiple sclerosis, uveitis, rheumatoid
 CC disease, etc.. Reducing CD28 expression may reduce the effects of
 CC antigenic stimulation of CD28 positive T cells, with a consequent
 CC reduction in cytokine release.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;
 SQ Query Match 82.2%; Score 14.8; DB 17; Length 18;
 Best Local Similarity 88.9%; Pred. No. 7.6e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 TTGGAGGGGGAGGAGGGG 18
 DB 1 TTGGAGGGGGTGTGGGG 18
 RESULT 11
 AAX90328
 ID AAX90328 standard; DNA; 18 BP.
 XX AAX90328;
 XX 24-SEP-1999 (first entry)
 XX CD28 inhibiting phosphorothioate oligonucleotide RT03S.
 XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
 XX immune system mediated disease; gamma-interferon; IL-8;
 XX phosphorothioate; ss.
 XX Synthetic.
 XX US5932556-A.
 XX 03-AUG-1999.
 XX 18-SEP-1995; 95US-0529878.
 XX 18-SEP-1995; 95US-0529878.
 XX (TAMR/) TAM R C.
 XX Tam RC;
 XX WPI; 1999-443609/37.
 XX Query Match 82.2%; Score 14.8; DB 17; Length 18;
 Best Local Similarity 88.9%; Pred. No. 7.6e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 TTGGAGGGGGAGGAGGGG 18
 DB 1 TTGGAGGGGGTGTGGGG 18
 RESULT 12
 AAX90290
 ID AAX90290 standard; DNA; 18 BP.
 XX AAX90290;
 XX 24-SEP-1999 (first entry)
 XX CD28 inhibition oligonucleotide RT03.
 XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
 XX immune system mediated disease; gamma-interferon; IL-8; ss.
 XX Synthetic.
 XX US5932556-A.
 XX 03-AUG-1999.
 XX 18-SEP-1995; 95US-0529878.
 XX 18-SEP-1995; 95US-0529878.
 XX (TAMR/) TAM R C.
 XX Tam RC;
 XX WPI; 1999-443609/37.
 XX Treatment of immune system-mediated diseases by inhibiting
 PT expression of CD28, IL-2, gamma-interferon or IL-8
 XX Claim 5; Column 29; 45pp; English.
 XX The present invention describes a method for inhibiting the expression
 CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
 CC comprises subcutaneous administration of an oligonucleotide (OGN).
 CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
 CC method. The OGNs are used for the treatment of immune system-mediated
 CC diseases. The present sequence represents a CD28 inhibiting
 CC phosphorothioate oligonucleotide used in the exemplification of the
 CC present invention.
 XX Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;
 SQ Query Match 82.2%; Score 14.8; DB 20; Length 18;
 Best Local Similarity 88.9%; Pred. No. 7.6e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 TTGGAGGGGGAGGAGGGG 18
 DB 1 TTGGAGGGGGTGTGGGG 18
 RESULT 12
 AAX90290
 ID AAX90290 standard; DNA; 18 BP.
 XX AAX90290;
 XX 24-SEP-1999 (first entry)
 XX CD28 inhibition oligonucleotide RT03.
 XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
 XX immune system mediated disease; gamma-interferon; IL-8; ss.
 XX Synthetic.
 XX US5932556-A.
 XX 03-AUG-1999.
 XX 18-SEP-1995; 95US-0529878.
 XX 18-SEP-1995; 95US-0529878.
 XX (TAMR/) TAM R C.
 XX Tam RC;
 XX WPI; 1999-443609/37.
 XX Treatment of immune system-mediated diseases by inhibiting
 PT expression of CD28, IL-2, gamma-interferon or IL-8
 XX Claim 5; Column 29; 45pp; English.
 XX The present invention describes a method for inhibiting the expression
 CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
 CC comprises subcutaneous administration of an oligonucleotide (OGN).
 CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
 CC method. The OGNs are used for the treatment of immune system-mediated
 CC diseases. The present sequence represents a CD28 inhibiting
 CC phosphorothioate oligonucleotide used in the exemplification of the
 CC present invention.
 XX Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;
 SQ Query Match 82.2%; Score 14.8; DB 20; Length 18;
 Best Local Similarity 88.9%; Pred. No. 7.6e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 TTGGAGGGGGAGGAGGGG 18
 DB 1 TTGGAGGGGGTGTGGGG 18

PT Treatment of immune system-mediated diseases by inhibiting
 PT expression of CD28, IL-2, gamma-interferon or IL-8
 XX Example; Column 21; 45pp; English.
 XX The present invention describes a method for inhibiting the expression
 CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
 CC comprises subcutaneous administration of an oligonucleotide (OGN).
 CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
 CC method. The OGNs are used for the treatment of immune system-mediated
 CC diseases. The present sequence represents a CD28 inhibiting
 CC phosphorothioate oligonucleotide used in the exemplification of the
 CC present invention.
 XX Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;
 SQ Query Match 82.2%; Score 14.8; DB 20; Length 18;
 Best Local Similarity 88.9%; Pred. No. 7.6e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 TTGGAGGGGGAGGAGGGG 18
 DB 1 TTGGAGGGGGTGTGGGG 18
 RESULT 12
 AAX90290
 ID AAX90290 standard; DNA; 18 BP.
 XX AAX90290;
 XX 24-SEP-1999 (first entry)
 XX CD28 inhibition oligonucleotide RT03.
 XX CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
 XX immune system mediated disease; gamma-interferon; IL-8; ss.
 XX Synthetic.
 XX US5932556-A.
 XX 03-AUG-1999.
 XX 18-SEP-1995; 95US-0529878.
 XX 18-SEP-1995; 95US-0529878.
 XX (TAMR/) TAM R C.
 XX Tam RC;
 XX WPI; 1999-443609/37.
 XX Treatment of immune system-mediated diseases by inhibiting
 PT expression of CD28, IL-2, gamma-interferon or IL-8
 XX Claim 5; Column 29; 45pp; English.
 XX The present invention describes a method for inhibiting the expression
 CC of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method
 CC comprises subcutaneous administration of an oligonucleotide (OGN).
 CC AAX90288 to AAX90291 represent specifically claimed OGNs for use in the
 CC method. The OGNs are used for the treatment of immune system-mediated
 CC diseases. The present sequence represents a CD28 inhibiting
 CC phosphorothioate oligonucleotide used in the exemplification of the
 CC present invention.
 XX Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;
 SQ Query Match 82.2%; Score 14.8; DB 20; Length 18;
 Best Local Similarity 88.9%; Pred. No. 7.6e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 TTGGAGGGGGAGGAGGGG 18
 DB 1 TTGGAGGGGGTGTGGGG 18

Db 1 TTGGAGGGGGTGGTGGG 18

RESULT 13

AAZ99625
ID AAZ99625 standard; DNA; 18 BP.

XX AC AAZ99625;

XX DT 12-JUL-2000 (first entry)

XX DE Nucleotide sequence of G-motif oligonucleotide GRI.

XX G-motif oligonucleotide; vaccine; Toxoplasmosis; viral infection;
KW antigen presenting cell activation; natural killer cell; septic shock;
KW cytotoxic T-lymphocyte; inflammation; autoimmune disease;
KW rheumatoid arthritis; Crohn's disease; sarcoidosis; multiple sclerosis;
KW Kawasaki syndrome; graft-versus-host disease; transplant rejection;
KW helper T cell response 1-mediated disease; Lyme arthritis;
KW Streptococcal induced arthritis; chronic inflammatory bowel disease;
KW psoriasis vulgaris; experimental allergic encephalomyelitis;
KW insulin-dependent diabetes mellitus; bacterial infection;
KW parasitic infection; Leishmaniasis; spontaneous abortion; tumour; ss.

XX OS Synthetic.

XX PN WO200014217-A2.

XX PD 16-MAR-2000.

XX PF 03-SEP-1999; 99WO-EP06502.

XX PR 03-SEP-1998; 98EP-0116652.

XX PA (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.

XX PI Wagner H, Lipford GB, Heeg K;

XX DR WPI; 2000-256970/22.

XX PT Compositions comprising G-motif oligonucleotides useful for treating
e.g. septic shock, rheumatoid arthritis, diabetes and human
immunodeficiency virus infections -

XX PS Example 14; Page 32; 75pp; English.

XX The present sequence represents a G-motif oligonucleotide of the
invention. The specification describes compositions comprising G-motif
oligonucleotides. The G-motif oligonucleotides inhibit activation of
antigen presenting cells by inhibiting the uptake of DNA by a cell, by
stimulating natural killer cells, or by co-stimulating cytotoxic
T-lymphocytes. The G-motif oligonucleotides may be used for the
production of vaccines for treating septic shock, inflammation,
autoimmune diseases (e.g. rheumatoid arthritis, Crohn's disease,
sarcoidosis, multiple sclerosis, Kawasaki syndrome, graft-versus-host
disease and transplant rejection), helper T cell response 1-mediated
diseases (e.g. Streptococcal induced arthritis, Lyme arthritis, chronic
inflammatory bowel disease, psoriasis vulgaris, experimental allergic
encephalomyelitis, and insulin-dependent diabetes mellitus), bacterial
infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis),
viral infections (e.g. Cytomegalovirus and human immunodeficiency virus
(HIV)-infections), spontaneous abortions and tumours. They may also be
used to induce proliferation of bone marrow cells, especially macrophage
precursor cells.

XX SQ Sequence 18 BP; 1 A; 0 C; 13 G; 4 T; 0 other;

Query Match 82.2%; Score 14.8; DB 21; Length 18;

Best Local Similarity 88.9%; Pred. No. 7.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGGAGGGGG 18

Db 1 TTGGAGGGGGTGGTGGG 18

RESULT 14

AAZ99650/c
ID AAZ99650 standard; DNA; 18 BP.

XX AC AAZ99650;

XX DT 12-JUL-2000 (first entry)

XX DE Nucleotide sequence of non-G-motif oligonucleotide GRF1comp.

XX G-motif oligonucleotide; vaccine; Toxoplasmosis; viral infection;
KW antigen presenting cell activation; natural killer cell; septic shock;
KW cytotoxic T-lymphocyte; inflammation; autoimmune disease;
KW rheumatoid arthritis; Crohn's disease; sarcoidosis; multiple sclerosis;
KW Kawasaki syndrome; graft-versus-host disease; transplant rejection;
KW helper T cell response 1-mediated disease; Lyme arthritis;
KW Streptococcal induced arthritis; chronic inflammatory bowel disease;
KW psoriasis vulgaris; experimental allergic encephalomyelitis;
KW insulin-dependent diabetes mellitus; bacterial infection;
KW parasitic infection; Leishmaniasis; spontaneous abortion; tumour; ss.

XX OS Synthetic.

XX PN WO200014217-A2.

XX PD 16-MAR-2000.

XX PF 03-SEP-1999; 99WO-EP06502.

XX PR 03-SEP-1998; 98EP-0116652.

XX PA (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.

XX PI Wagner H, Lipford GB, Heeg K;

XX DR WPI; 2000-256970/22.

XX PT Compositions comprising G-motif oligonucleotides useful for treating
e.g. septic shock, rheumatoid arthritis, diabetes and human
immunodeficiency virus infections -

XX PS Example 14; Page 32; 75pp; English.

XX The present sequence represents a non-G-motif oligonucleotide of the
invention. The specification describes compositions comprising G-motif
oligonucleotides. The G-motif oligonucleotides inhibit activation of
antigen presenting cells by inhibiting the uptake of DNA by a cell, by
stimulating natural killer cells, or by co-stimulating cytotoxic
T-lymphocytes. The G-motif oligonucleotides may be used for the
production of vaccines for treating septic shock, inflammation,
autoimmune diseases (e.g. rheumatoid arthritis, Crohn's disease,
sarcoidosis, multiple sclerosis, Kawasaki syndrome, graft-versus-host
disease and transplant rejection), helper T cell response 1-mediated
diseases (e.g. Streptococcal induced arthritis, Lyme arthritis, chronic
inflammatory bowel disease, psoriasis vulgaris, experimental allergic
encephalomyelitis, and insulin-dependent diabetes mellitus), bacterial
infections, parasitic infections (e.g. Leishmaniasis or Toxoplasmosis),
viral infections (e.g. Cytomegalovirus and human immunodeficiency virus
(HIV)-infections), spontaneous abortions and tumours. They may also be
used to induce proliferation of bone marrow cells, especially macrophage
precursor cells.

XX SQ Sequence 18 BP; 4 A; 13 C; 0 G; 1 T; 0 other;

Query Match 82.2%; Score 14.8; DB 21; Length 18;

Best Local Similarity 88.9%; Pred. No. 7.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTGGAGGGGGGAGGGGG 18

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Db      18 TTGGAGGGGGTGTGGGG 1
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RESULT 15
AAT36197
ID AAT36197 standard; DNA; 21 BP.
XX
XX AAT36197;
XX
XX 25-MAR-2003 (updated)
DT 15-APR-1997 (first entry)
XX
XX DE Triplex forming oligo targeting CD28 5'-UTR (nt 58-78).
XX
XX Reduction; T cell; CD28; Gene expression; treatment; immune system;
XX disorder; graft versus host disease; septic shock; viral disease;
XX psoriasis; type I diabetes mellitus; thyroiditis; sarcoides;
XX multiple sclerosis; uveitis; rheumatoid arthritis; 5'-UTR;
XX systemic lupus erythematosus; inflammatory bowel disease;
XX triplex forming; oligonucleotide; 5'-untranslated region; ss
XX
XX OS Synthetic.
XX
XX PN WO9624380-A1.
XX
XX PD 15-AUG-1996.
XX
XX PF 05-FEB-1996; 96WO-US01507.
XX
XX PR 09-FEB-1995; 95US-0387041.
XX PR 18-SEP-1995; 95US-0529878.
XX PR 09-FEB-1995; 95US-0387041.
XX PR 18-SEP-1995; 95US-0529878.
XX
XX PA (ICNC ) ICN PHARM INC.
XX
XX PI Tam RC;
XX
XX DR WPI; 1996-384228/38.
XX
XX PT Oligo:nucleotide which reduces CD28 gene expression in T cells -
XX for treating immune system diseases, e.g. graft vs. host disease,
XX septic shock, psoriasis, etc.
XX
XX PS Claim 10; Page 54; 77pp; English.
XX
XX CC The present oligonucleotide reduces T cell CD28 gene expression,
XX useful in the treatment of CD28 mediated diseases, particularly
XX immune system disorders, e.g. graft versus host disease, septic
XX shock, viral disease, psoriasis, type I diabetes mellitus,
XX thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid
XX arthritis, systemic lupus erythematosus, inflammatory bowel
XX disease, etc. Reducing CD28 expression may reduce the effects of
XX antigenic stimulation of CD28 positive T cells, with a consequent
XX reduction in cytokine release.
XX CC (Updated on 25-MAR-2003 to correct PR field.)
XX
XX SQ Sequence 21 BP; 1 A; 0 C; 16 G; 4 T; 0 other;
Query Match 82.2%; Score 14.8; DB 17; Length 21;
Best Local Similarity 88.9%; Fred. NO. 7.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1 TTGGAGGGGGGAGGGGGG 18
|||||
Db      4 TTGGAGGGGGTGTGGGG 21
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Search completed: October 27, 2003, 11:25:20
 Job time : 163 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:32:29 ; Search time 376.114 Seconds
(without alignments)
1957.844 Million cell updates

Title: US-09-331-204A-8

Perfect score: 18
Sequence:

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 681044

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Minimum DB seq length: 0
Maximum DB seq length: 22
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *

4: gb_ba: *
5: gb_htg: *
6: gb_in: *
7: gb_om: *
8: gb_ov: *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	16.4	91.1	18	6	AX023402	Sequence	
C	2	16.4	91.1	18	AX023427	Sequence	
	3	13.8	76.7	20	AX18779	Sequence	
	4	13.8	76.7	21	A31974	Synthetic H	
5	13.8	76.7	21	BD131393	Sequence		
C	6	13.8	76.7	21	BD001798	Immunogen	
	7	13.4	74.4	17	AX532425	Sequence	
C	8	13.4	74.4	17	AX532426	Sequence	
	9	13.4	74.4	17	AX532427	Sequence	
10	13.4	74.4	19	AX477615	Sequence		
11	13.4	74.4	19	AX505035	Sequence		
12	13.4	74.4	19	I28584	Sequence 37		
13	13.4	74.4	19	I58745	Sequence 37		
C	14	13.4	74.4	20	AR297574	Sequence	
	15	13.3	72.2	20	AX662935	Sequence	
C	16	12.8	71.1	17	AR029938	Sequence	
C	17	12.8	71.1	17	AX214603	Sequence	
	18	12.8	71.1	17	AX214542	Sequence	
19	12.8	71.1	18	AR055448	Sequence		
20	12.8	71.1	18	AX600765	Sequence		
21	12.8	71.1	18	E04543	linker. 9/1		
C	22	12.8	71.1	20	AR212973	Sequence	
	23	12.8	71.1	20	AX418780	Sequence	
C	24	12.8	71.1	20	BD177744	A method	
	25	12.8	71.1	21	AR061827	Sequence	
26	12.8	71.1	21	AR252818	Sequence		
C	27	12.4	68.9	17	AX532424	Sequence	
	28	12.4	68.9	17	AX532428	Sequence	
29	12.4	68.9	22	AX188499	Sequence		
C	30	12.2	67.8	17	AX235037	Sequence	
	31	12.2	67.8	17	AX532447	Sequence	
C	32	12.2	67.8	18	A02165	Nucleotide	
C	33	12.2	67.8	18	A04686	Nucleotide	
C	34	12.2	67.8	19	AR012711	Sequence	
C	35	12.2	67.8	19	AR036657	Sequence	
C	36	12.2	67.8	19	AR088921	Sequence	
	37	12.2	67.8	19	AR152368	Sequence	
38	12.2	67.8	20	AR012712	Sequence		
C	39	12.2	67.8	20	AR036658	Sequence	
	40	12.2	67.8	20	AR088922	Sequence	
41	12.2	67.8	20	AR152369	Sequence		
42	12.2	67.8	20	AR232303	Sequence		
43	12.2	67.8	20	AX468033	Sequence		
44	12.2	67.8	20	BD138339	Antisense		
45	12.2	67.8	21	AX023422	Sequence		

ALIGNMENTS

RESULT 1

AX023402

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

DISCUSSION

REFERENCE

AUTHORS

TITLE
 TO BE PRINTED
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 TITLE PAGE OF THE
 REPORT

AX023402	18 bp	DNA	linear	PAT 15-SEP-2000
Sequence	17 from Patent WO0014217.			

AX023402 1 GT.10193903

AX023402.1 GI:101838

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Lipford, G. B., Heeg, K. and Wagner, H.

G-motif oligonucleotides and uses th

Patent: WO 0014217-A 17 16-MAR-2000;

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CPG IMMUNOPHARMACEUTICALS GMBH (DE)
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QY
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LOCUS
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DEFINITION
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ACCESSION
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VERSION
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KEYWORDS
  synthetic construct
  synthetic construct
  artificial sequences.
SOURCE
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REFERENCE
  Lipford,G.B., Heeg,K. and Wagner,H.
  G-motif oligonucleotides and uses thereof
  Patent: WO 0014217-A 42 16-MAR-2000;
  LIPFORD GRAYSON B (DE); HEEG KLAUS (DE); WAGNER HERMANN (DE);
  CPG IMMUNOPHARMACEUTICALS GMBH (DE)
FEATURES
  source
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QY
  1 TTGGAGGGGGAGGTGGGG 18
  |||||
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  |||||

RESULT 3
AX418779
LOCUS
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DEFINITION
  Sequence 174 from Patent WO0210378.
ACCESSION
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VERSION
  AX418779.1 GI:21523642
KEYWORDS
  synthetic construct
  synthetic construct
  artificial sequences.
SOURCE
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REFERENCE
  Cowsett,L.M., Wyatt,J., Freier,S.M., Monia,B.P., Butler,M.M. and
  McKay,R.
  Antisense modulation of ptp1b expression
  Patent: WO 0210378-A 174 07-FEB-2002;
  ISIS PHARMACEUTICALS, INC. (US)
FEATURES
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CPG IMMUNOPHARMACEUTICALS GMBH (DE)
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Matches
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QY
  2 TGGAGGGGGAGGTGGGG 18
  |||||
  1 TGGCCGGGGAGGTGGGG 17
  |||||

RESULT 4
A31974
LOCUS
  A31974
DEFINITION
  Synthetic HIV-1/2 diagnosis primer.
ACCESSION
  A31974
VERSION
  A31974.1 GI:1567257
KEYWORDS
  synthetic construct
  synthetic construct
  artificial sequences.
SOURCE
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REFERENCE
  1 (bases 1 to 21)
  Moncany,M. and Montagnier,L.
  Nucleotide sequences of retroviral genomes of types HIV-1, HIV-2
  and SIV, their uses for the amplification of these genomes and
  diagnosis in vitro of these viral infections
  Patent: EP 0403333-A 29 19-DEC-1990;
  INSTITUT PASTEUR; INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE
  MEDICALE (INSERM)
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ORIGIN
  5 a 2 c 13 g 1 t

Query Match
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Best Local Similarity
  88.2%; Pred. No. 2.6e+05;
Matches
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QY
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  |||||
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RESULT 5
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LOCUS
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DEFINITION
  Sequence 45 from patent US 6194142.
ACCESSION
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VERSION
  AR131393.1 GI:14120296
KEYWORDS
  Unknown.
SOURCE
  Unknown.
REFERENCE
  1 (bases 1 to 21)
  Moncany,M. and Montagnier,L.
  Nucleotide sequences derived from the genome of retroviruses of the
  HIV-1, HIV-2, and SIV type, and their uses in particular for the
  amplification of the genomes of these retroviruses and for the in
  vitro diagnosis of the diseases due to these viruses
  Patent: US 6194142-A 45 27-FEB-2001;
  Location/Qualifiers
    1..21
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BASE COUNT
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ORIGIN
  5 a 2 c 13 g 1 t

Query Match
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Best Local Similarity 88.2%; Pred. No. 2.6e+05; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGGAGGGGAGGTGGG 18
Db 3 TGGAGGGGAGGAGGAG 19

RESULT 6
BD001798
LOCUS 21 bp DNA linear PAT 31-JAN-2002
DEFINITION Immunogenic compounds containing a translation product of nucleotide sequence from retrovirus genome of HIV-1, HIV-2 and SIV types
ACCESSION BD001798
VERSION BD001798.1 GI:18626357
KEYWORDS JP 2000093187-A/45.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 21)
AUTHORS Moncany, M. and Montagnier, L.
TITLE Immunogenic compounds containing a translation product of nucleotide sequence from retrovirus genome of HIV-1, HIV-2 and SIV types
JOURNAL Patent: JP 2000093187-A 45 04-APR-2000;
COMMENT INST PASTEUR, INST NATL DE LA SANTE & DE LA RECHERCHE MEDICAL
OS Artificial Sequence
PN JP 2000093187-A/45
PD 04-APR-2000
PF 24-SEP-1999 JP 1999270165
PR 02-JUN-1989 FR 89/07354, 20-SEP-1989 FR 89/12371 PI
MAURICE MONCANY, LUC MONTAGNIER
PC C12N15/09, A61K39/21, A61K48/00, A61P31/18, C07H21/04, C07K14/155,
PC C07K14/16
PC C12Q1/68, C12Q1/70, G01N33/569, C12N15/00
CC
FH Key
FT source
FT Location/Qualifiers
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/organism="Artificial Sequence".

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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

BASE COUNT
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ORIGIN
1 t

Query Match 75.7%; Score 13.8; DB 6; Length 21;
Best Local Similarity 88.2%; Pred. No. 2.6e+05; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGGAGGGGAGGTGGG 18
Db 3 TGGAGGGGAGGAGGAG 19

RESULT 7
AX532425/c
LOCUS 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1934 from Patent EP1239051.
ACCESSION AX532425
VERSION AX532425.1 GI:25256625
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon, M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1934 11-SEP-2002;
Aeomica, Inc. (US)

FEATURES
source
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/organism="Homo sapiens"
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BASE COUNT
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ORIGIN
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Query Match 74.4%; Score 13.4; DB 6; Length 17;
Best Local Similarity 93.3%; Pred. No. 4e+05; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAGGGGAGGTGGG 18
Db 17 GAGGGGAGGAGGG 3

RESULT 8
AX532426/c
LOCUS 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1935 from Patent EP1239051.
ACCESSION AX532426
VERSION AX532426.1 GI:25256627
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon, M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1935 11-SEP-2002;
Aeomica, Inc. (US)

FEATURES
source
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/organism="Homo sapiens"
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BASE COUNT
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ORIGIN
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Query Match 74.4%; Score 13.4; DB 6; Length 17;
Best Local Similarity 93.3%; Pred. No. 4e+05; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAGGGGAGGTGGG 18
Db 16 GAGGGGAGGAGGG 2

RESULT 9
AX532427/c
LOCUS 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1936 from Patent EP1239051.
ACCESSION AX532427
VERSION AX532427.1 GI:25256629
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon, M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1936 11-SEP-2002;
Aeomica, Inc. (US)

FEATURES
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/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT
1 a 12 c 1 g 3 t

ORIGIN
1 a 12 c 0 g 4 t

Query Match 74.4%; Score 13.4; DB 6; Length 17;
Best Local Similarity 93.3%; Pred. No. 4e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAGGGGAGGTGGG 18
|||||
Db 15 GAGGGGAGGAGGG 1

RESULT 10
LOCUS AX477615 19 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 67 from Patent WO0246433.
ACCESSION AX477615
VERSION AX477615.1 GI:22216795
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Saus, J.
TITLE Tnf-inducible promoters and methods for using
JOURNAL Patent: WO 0246433-A 67 13-JUN-2002;
Saus, Juan (ES)
FEATURES
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Location/Qualifiers
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/db_xref="taxon:32630"
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BASE COUNT 3 a 2 c 11 g 3 t
ORIGIN

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Best Local Similarity 93.3%; Pred. No. 3.9e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TCGAGGGGAGGTGG 16
|||||
Db 5 TCGAGGAGGAGGTGG 19

RESULT 11
AX505035
LOCUS AX505035 19 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 67 from Patent WO0246378.
ACCESSION AX505035
VERSION AX505035.1 GI:23386357
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Saus, J.
TITLE Alternative pol k nucleotide and amino acid sequence and methods for using
JOURNAL Patent: WO 0246378-A 67 13-JUN-2002;
Saus, Juan (ES)
FEATURES
source
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BASE COUNT 3 a 2 c 11 g 3 t
ORIGIN

Query Match 74.4%; Score 13.4; DB 6; Length 19;
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Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TCGAGGGGAGGTGG 16
|||||
Db 5 TCGAGGAGGAGGTGG 19

RESULT 12
LOCUS I28584 19 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 37 from patent US 5571937.
ACCESSION I28584
VERSION I28584.1 GI:1819360
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Watanabe, K.A., Ren, W.-Y. and Weil, R.
TITLE Complementary DNA and toxins
JOURNAL Patent: US 5571937-A 37 05-NOV-1996;
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Location/Qualifiers
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Query Match 74.4%; Score 13.4; DB 6; Length 19;
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QY 3 GGAGGGGAGGTGGG 17
|||||
Db 5 GGAGGAGGAGGTGGG 19

RESULT 13
LOCUS I58746 19 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 37 from patent US 5652350.
ACCESSION I58746
VERSION I58746.1 GI:2477984
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Watanabe, K.A., Ren, W.-Y. and Weil, R.
TITLE Complementary DNA and toxins
JOURNAL Patent: US 5652350-A 37 29-JUL-1997;
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Query Match 74.4%; Score 13.4; DB 6; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.9e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGGGAGGTGGG 17
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Db 5 GGAGGAGGAGGTGGG 19

RESULT 14
LOCUS AR297674/c 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 9409 from patent US 6537751.
ACCESSION AR297674
VERSION AR297674.1 GI:31684958
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)

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Db 5 TCGAGGAGGAGGTGG 19

RESULT 12
LOCUS I28584 19 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 37 from patent US 5571937.
ACCESSION I28584
VERSION I28584.1 GI:1819360
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Watanabe, K.A., Ren, W.-Y. and Weil, R.
TITLE Complementary DNA and toxins
JOURNAL Patent: US 5571937-A 37 05-NOV-1996;
FEATURES
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Location/Qualifiers
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Query Match 74.4%; Score 13.4; DB 6; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.9e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGGGAGGTGGG 17
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Db 5 GGAGGAGGAGGTGGG 19

RESULT 13
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DEFINITION Sequence 37 from patent US 5652350.
ACCESSION I58746
VERSION I58746.1 GI:2477984
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Watanabe, K.A., Ren, W.-Y. and Weil, R.
TITLE Complementary DNA and toxins
JOURNAL Patent: US 5652350-A 37 29-JUL-1997;
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Best Local Similarity 93.3%; Pred. No. 3.9e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAGGGGAGGTGGG 17
|||||
Db 5 GGAGGAGGAGGTGGG 19

RESULT 14
LOCUS AR297674/c 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 9409 from patent US 6537751.
ACCESSION AR297674
VERSION AR297674.1 GI:31684958
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)

AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 9409 25-MAR-2003;
FEATURES Location/Qualifiers
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BASE COUNT 4 a 11 c 0 g 5 t
ORIGIN

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|||||
Db 17 TTGGAGGGGAGATG 3

RESULT 15
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LOCUS AX662935 20 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 22 from Patent WO02066681.
ACCESSION AX662935
VERSION AX662935.1 GI:29163516
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Poole,J., Roninson,I.B. and Chang,B.D.
TITLE Reagents and methods for identifying and modulating expression of
genes regulated by cdk inhibitors
JOURNAL Patent: WO 02066681-A 22 29-AUG-2002;
THE BOARD OF TRUSTEES OF THE UNIVERSITY OF ILLINOIS (US)
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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IIa)"

BASE COUNT 4 a 0 c 12 g 4 t
ORIGIN

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGGGAGGTGGG 17
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Db 1 AGGGGAGGTGGG 13

Search completed: October 27, 2003, 11:09:27
Job time : 377.114 secs